



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 7 : C07H 21/04, C07K 14/00, C12N 15/85	A1	(11) International Publication Number: WO 00/32618 (43) International Publication Date: 8 June 2000 (08.06.00)
(21) International Application Number: PCT/US99/28315 (22) International Filing Date: 30 November 1999 (30.11.99) (30) Priority Data: 09/201,227 30 November 1998 (30.11.98) US (71) Applicant: EXELIXIS PHARMACEUTICALS, INC. [US/US]; 260 South Littlefield Avenue, South San Francisco, CA 94080 (US). (72) Inventors: KEYES, Linda, N.; 46 Madera Avenue, San Carlos, CA 94070 (US). DOBERSTEIN, Stephen, K.; 2 Townsend Street, San Francisco, CA 94107 (US). BUCHMAN, Andrew, R.; 3119 Eton Avenue, Berkeley, CA 94705 (US). REDDY, Bindu, P.; 885 Greenwich Street, San Francisco, CA 94133 (US). RUDDY, David, A.; 885 Greenwich Street, San Francisco, CA 94133 (US). (74) Agents: ANTLER, Adriane, M. et al.; Pennie & Edmonds LLP, 1155 Avenue of the Americas, New York, NY 10036 (US).		(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i>
(54) Title: NUCLEIC ACIDS AND POLYPEPTIDES OF <i>D. MELANOGASTER</i> INSULIN-LIKE GENES AND USES THEREOF		
(57) Abstract <p>The present invention relates to <i>D. melanogaster</i> insulin-like genes and methods for identifying insulin-like genes. The methods provide nucleotide sequences of <i>D. melanogaster</i> insulin-like genes, amino acid sequences of their encoded proteins, and derivatives (<i>e.g.</i>, fragments) and analogs thereof. The invention further relates to fragments (and derivatives and analogs thereof) of insulin-like proteins which comprise one or more domains of an insulin-like protein. Antibodies to an insulin-like protein, and derivatives and analogs thereof, are provided. Methods of production of an insulin-like protein (<i>e.g.</i>, by recombinant means), and derivatives and analogs thereof, are provided. Further, methods to identify the biological function of a <i>D. melanogaster</i> insulin-like gene are provided, including various methods for the functional modification (<i>e.g.</i>, overexpression, underexpression, mutation, knock-out) of one or more genes simultaneously. Still further, methods to identify a <i>D. melanogaster</i> gene which modifies the function of, and/or functions in a signaling pathway with an insulin-like gene are provided. The invention further provides uses of <i>Drosophila</i> insulin-like nucleic acids and proteins, <i>e.g.</i>, as media additives, and as pesticides.</p>		

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NUCLEIC ACIDS AND POLYPEPTIDES OF *D. MELANOGASTER* INSULIN-
LIKE GENES AND USES THEREOF

PRIORITY APPLICATION

This application claims priority to U.S. Ser. No. 09/201,227 (Keyes *et al.*) filed
5 November 30, 1998.

BACKGROUND OF THE INVENTION

Insulin is the central hormone governing metabolism in vertebrates (reviewed in
Steiner et al., 1989, In *Endocrinology*, DeGroot, eds. Philadelphia, Saunders: 1263-1289).
10 In humans, insulin is secreted by the beta cells of the pancreas in response to elevated
blood glucose levels which normally occur following a meal. The immediate effect of
insulin secretion is to induce the uptake of glucose by muscle, adipose tissue, and the liver.
A longer term effect of insulin is to increase the activity of enzymes that synthesize
glycogen in the liver and triglycerides in adipose tissue. Insulin can exert other actions
15 beyond these "classic" metabolic activities, including increasing potassium transport in
muscle, promoting cellular differentiation of adipocytes, increasing renal retention of
sodium, and promoting production of androgens by the ovary. Defects in the secretion
and/or response to insulin are responsible for the disease diabetes mellitus, which is of
enormous economic significance. Within the United States, diabetes mellitus is the fourth
20 most common reason for physician visits by patients; it is the leading cause of end-stage
renal disease, non-traumatic limb amputations, and blindness in individuals of working
age (Warram et al., 1995, In *Joslin's Diabetes Mellitus*, Kahn and Weir, eds., Philadelphia,
Lea & Febiger, pp. 201-215; Kahn et al., 1996, *Annu. Rev. Med.* 47:509-531; Kahn, 1998,
Cell 92:593-596). Beyond its role in diabetes mellitus, the phenomenon of insulin
25 resistance has been linked to other pathogenic disorders including obesity, ovarian
hyperandrogenism, and hypertension.

Insulin-like proteins are a large and widely-distributed group of structurally-related
peptide hormones that have pivotal roles in controlling animal growth, development,
reproduction, and metabolism. Consequently, the insulin superfamily has become one of
30 the most intensively investigated classes of peptide hormones. Studies of insulin-like

molecules in invertebrates have been motivated by the desire to identify proteins that play analogous roles to the well-characterized activities of insulin and IGF in mammals.

Although insulin superfamily members in invertebrates have been less extensively analyzed than in vertebrates, a number of different subgroups have been defined. Such

subgroups include molluscan insulin-related peptides (MIP-I to MIP-VII) (Smit et al., 1988, Nature 331:535-538; Smit et al., 1995, Neuroscience 70:589-596), the bombyxins of lepidoptera (originally referred to as prothoracicotrophic hormone or PTTH) (Kondo et al., 1996, J Mol. Biol. 259:926-937), and the locust insulin-related peptide (LIRP) (Lagueux et al., 1990, Eur. J. Biochem. 187:249-254). Most recently, there have been descriptions of

an exceptionally large insulin-like gene family in the nematode *C. elegans* (WO1999US08522; Duret, et al., 1998, Genome Res. 8:348-353; Brousseau, et al., 1998, Early 1998 East Coast Worm Meeting, abstract 20; Kawano, et al., 1998, Worm Breeder's Gazette 15(2):47; Pierce and Ruvkun, 1998, Early 1998 East Coast Worm Meeting, abstract 150; Wisotzkey and Liu, 1998, Early 1998 East Coast Worm Meeting, abstract 206). Also, putative orthologs of both vertebrate insulin and IGF have been identified in a tunicate (McRory and Sherwood, 1997, DNA and Cell Biology 116:939-949). From the extensive sequence divergence evident among known subfamilies of insulin-like proteins, it is assumed that this is an ancient family of regulatory hormones that evolved to control growth, reproduction and metabolism in early metazoans. However, the precise evolutionary origins of this important family remain unclear.

Early attempts to propagate *Drosophila* cells in culture revealed a growth factor requirement in defined medium which could be provided by purified bovine insulin, implying the existence of a related endogenous factor in. Also, bovine and human insulin were found to stimulate the differentiation of *Drosophila* cells grown in culture (Seecof and Dewhurst, 1974, Cell Differ. 3(1):63-70; Pimentel, et al., 1996, Biochem. Biophys. Res. Commun. 226(3):855-61). One report described the presence of an "insulin-like activity" in unpurified *Drosophila* extracts that elicited a hypoglycemic effect when injected into mice, although the activity was not particularly strong (Meneses and De Los Angeles Ortiz, 1975, Comp. Biochem. Physiol. A. 51(2):483-5). Another group (LeRoith, et al., 1981, Diabetes 30(1):70-6) fractionated an insulin-like material from *Drosophila* based on immunoreactivity and showed that this material had insulin-like activity on isolated rat adipocytes. Also, polyclonal antibodies raised against bovine/porcine insulin were used to localize insulin-immunoreactive material in *Drosophila* tissue (Gorczyca, et

al., 1993, J. Neurosci. 13(9):3692-704), and specific insulin-immunoreactive substances were detected at neuromuscular junctions and in the central nervous system. However, these substances were not characterized further to validate that they correspond to *bona fide* insulin proteins at the level of primary protein sequence. Indeed, despite this long history of phenomenological evidence for insulin-like activities, true insulin-like genes and proteins in *Drosophila* have not been identified and characterized at the sequence level.

More compelling evidence for evolutionary conservation of insulin-like signaling pathways in *Drosophila* has come from the identification of an apparent homolog of the insulin receptor (Petrizzelli et al., 1986, Proc. Natl. Acad. Sci. U.S.A. 83:4710-4714). One insulin receptor homolog has been characterized thus far in *Drosophila*, termed InR (insulin receptor) also known as DIR (*Drosophila* insulin receptor) (Ruan et al., 1995, J. Biol. Chem. 270:4236-4243), which exhibits extensive homology with vertebrate insulin and IGF receptors in both the extracellular ligand-binding domain and the intracellular tyrosine kinase domain. Genetic analysis of InR function in *Drosophila* has revealed that it is an essential gene with an apparent role in the development of the epidermis and nervous system, as well as growth control (Fernandez et al., 1995, EMBO J. 14:3373-3384). Flies that are homozygous for mutations in InR generally exhibit an embryonic lethal phenotype, but flies bearing certain heteroallelic combinations of InR mutations live to adulthood and the surviving animals have about 50% the normal body weight (Garafalo, Chen, et al., 1996, Endocrinology 137(3):846-56). This result is reminiscent of a similar phenotype observed in mutant mice lacking functional IGF-I receptor genes (Liu, et al., 1993, Cell 75(1):59-72). Aside from this potential role of InR in growth regulation, the role, if any, that InR may have in metabolic regulation in *Drosophila* remains unclear. The ligand binding specificity of InR has been examined using in vitro assays for receptor activation/phosphorylation, and competitive binding of test ligands compared to porcine insulin (Fernandez-Almonacid and Rosen, 1987, Mol. Cell Biol. 7(8):2718-27). Curiously, the results of this study indicated that InR binds vertebrate insulin, and does not apparently recognize vertebrate IGF-I or IGF-II, or even bombyxin-II from the silkworm, implying that the natural *Drosophila* ligands for InR may bear more structural resemblance to vertebrate insulin than to these other insulin superfamily proteins.

The structural homologies of components of the *Drosophila* InR pathway with those involved in insulin signaling in mammals, as well as the function of the InR pathway

in controlling growth, and the circumstantial evidence for *Drosophila* insulin-like activities, raise critical questions with respect to further analysis of this pathway and its potential applications. Important issues regarding the biological function, regulation, and signaling mechanisms of insulin superfamily hormones could best be addressed if these pathways could be analyzed using model genetic organisms. In particular, the facile genetic tools currently available in two model organisms, the fruit fly *Drosophila melanogaster* and the nematode *Caenorhabditis elegans*, have proven to be of enormous utility in defining the biological function of genes through mutational analysis, as well as for identifying the components of biochemical pathways conserved during evolution with large-scale, systematic genetic screens (Scangos, 1997, Nature Biotechnol. 15:1220-1221; Miklos and Rubin, 1996, Cell 86:521-529). Key discoveries regarding constituents of a number of important human disease pathways, such as the Ras pathway and the pathway controlling programmed cell death, first came from genetic analysis of pathways known to have an evolutionary relation in *Drosophila* and *C. elegans*, and later shown to have direct relevance to human biology (Yuan et al., 1993, Cell 75:641-652; Therrien et al., 1995, Cell 83:879-888; Karim et al., 1996, Genetics 143:315-329; Kornfeld et al., 1995, Cell 83:903-913; Rubin et al., 1997, "Protein kinase required for Ras signal transduction", U.S. Patent No. 5,700,675; Steller et al., 1997, "Cell death genes of *Drosophila melanogaster* and vertebrate homologs", U.S. Patent No. 5,593,879).

SUMMARY OF THE INVENTION

The present invention relates to proteins encoded by nucleotide sequences of *D. melanogaster* insulin-like genes, as well as fragments and other derivatives and analogs of such insulin-like proteins. Nucleic acids encoding the insulin-like gene and fragments or derivatives are also within the scope of the invention. Production of the foregoing proteins, e.g., by recombinant methods, is provided.

The invention also relates to insulin-like protein derivatives and analogs which are functionally active, i.e., which are capable of displaying one or more known functional activities associated with a full-length (wild-type) insulin-like protein. Examples of such functional activities include antigenicity (ability to bind, or to compete for binding, to an anti-insulin-like protein antibody), immunogenicity (ability to generate antibody which binds to an insulin-like protein), and ability to bind (or

compete for binding) to a receptor for insulin (*e.g.*, that is encoded by the *D. melanogaster* insulin receptor-like gene, *InR*).

The invention further relates to fragments (and derivatives and analogs thereof) of an insulin-like protein which comprise one or more domains of the insulin-like protein.

Antibodies to an insulin-like protein, its derivatives and analogs, are additionally provided.

Methods for genetic analysis of pathways involving insulin superfamily hormones in *Drosophila* are provided. Such methods may yield results of importance to human disease. For example, systematic identification of participants in intracellular signaling by insulin-like hormones, or components regulating secretion and turnover of insulin-like hormones, provide leads to the identification of drug targets, therapeutic proteins, diagnostics, or prognostics useful for treatment or management of insulin resistance in diabetics.

BRIEF DESCRIPTION OF FIGURES

FIG. 1 illustrates the structural organization of precursor forms of the insulin superfamily of hormones. The different domains that make up precursor forms of insulin-like hormones are represented as boxes labeled Pre, F, B, C, A, D, and E. Domains that may remain in a mature hormone are represented as unshaded boxes (the B, A, and D peptide domains) or as lightly hatched (the C or "connecting" peptide domain). Domains that are removed during proteolytic processing are represented as shaded (the Pre peptide domain and F domain) or as hatched (the E peptide domain). IGF hormones are unique in having D and E peptide domains; these domains are represented as smaller boxes in FIG. 1. Cleavage sites utilized by proteases during proteolytic processing (*i.e.*, protein maturation) are indicated below the boxes. The asterisk marks the position of cleavage by signal peptidase. Arrows indicate cleavage sites by prohormone convertases. Disulfide bonds (S-S) are represented above the boxes with lines indicating connections between covalently-bonded Cys residues.

FIG. 2 illustrates conserved structural features of known insulin superfamily members. The aligned sequences of the B and A chain peptide domains are shown for representative insulin superfamily hormones from the following vertebrates and invertebrates: human insulin (Bell et al., 1979, Nature 29:525-527), human IGF-I (Jansen et al., 1983, Nature 306:609-611), human relaxin 1 (Hudson et al., 1983, Nature

301:628-631), RLF from human (Adham et al., 1993, J. Biol. Chem. 268:26668-26672),
placentin from human (Chassin et al., 1995, Genomics 29:465-470), bombyxin II from
silkworm (Nagasawa et al., 1986, Proc. Natl. Acad. Sci. U.S.A. 83:5840-5843), MIP from
freshwater snail (Smit et al., 1988, Nature 331:535-538), and LIRP from locust (Lagueux
5 et al., 1990, Eur. J. Biochem. 187:249-254). The numbering scheme shown at the bottom
of the figure is for residues of the A and B chains relative to residue numbers for human
insulin peptide domains. The nearly invariant positions of the six Cys residues that
participate in disulfide bonds are boxed. MIP-I is unusual in having two extra Cys
residues which are also individually boxed in that sequence. Other conserved amino acid
10 positions that play important roles in promoting the common insulin superfamily fold are
highlighted by shading of the following residue positions: B6, B8, B11, B15, B18, A2,
A16, and A19. Three helical regions that comprise the common insulin fold are marked
above the alignments using a "<--->" symbol.

FIG. 3 shows a gene map of *Drosophila* insulin-like gene cluster region, including
15 location and orientation of coding regions of dIns1, dIns2, dIns3, and dIns4. Units in kbp
indicate kilobase pairs of genomic DNA.

FIG. 4A-4P shows the annotated genomic DNA sequence of *D. melanogaster*
insulin-like gene cluster. Genomic sequence is set forth in SEQ ID NO:7.

FIG. 5 shows annotated sequence of *D. melanogaster* insulin-like protein dIns2 and
20 corresponding cDNA. dIns2 protein sequence is set forth in SEQ ID NO:2. dIns2 nucleic
acid sequence is set forth in SEQ ID NO:1.

FIG. 6 shows annotated sequence of *D. melanogaster* insulin-like protein dIns3 and
corresponding cDNA. dIns3 protein sequence is set forth in SEQ ID NO:4. dIns3 nucleic
acid sequence is set forth in SEQ ID NO:3.

FIG. 7 shows annotated sequence of *D. melanogaster* insulin-like protein dIns4 and
25 corresponding cDNA. dIns4 protein sequence is set forth in SEQ ID NO:6. dIns4 nucleic
acid sequence is set forth in SEQ ID NO:5.

FIG. 8 shows key structural features for *D. melanogaster* Insulin-like protein
folding and conserved Cysteine residues in vertebrate superfamily. Numbers shown in
30 parentheses represents the number of residues omitted from the C peptide sequence.

DETAILED DESCRIPTION OF THE INVENTION

Described herein are novel insulin-like genes from *Drosophila* and the characterization of their function. The *Drosophila* insulin-like genes described herein are a tightly clustered array encoding proteins that are much closer in structure to vertebrate insulins than the insulin-like proteins found in the nematode *C. elegans*.

5 Nonetheless, the *Drosophila* insulin-like proteins exhibit significant sequence diversity. These new insulin-like genes in *Drosophila* constitute very useful tools for probing the function and regulation of their corresponding pathways. Systematic genetic analysis of signaling pathways involving insulin-like proteins in *Drosophila* can be expected to lead to the discovery of new drug targets, therapeutic proteins, diagnostics and
10 prognostics useful in the treatment of diseases and clinical problems associated with the function of insulin superfamily hormones in humans and other animals, as well as clinical problems associated with aging and senescence. Furthermore, analysis of these same pathways using *Drosophila* insulin-like proteins as tools will have utility for identification and validation of pesticide targets in invertebrate pests that are
15 components of these signaling pathways.

Use of *Drosophila* insulin-like genes for such purposes as disclosed herein, has advantages over manipulation of other known components of the fruit fly InR pathway including *InR*, *Pi3K92E*, and *chico*. First, use of ligand-encoding *Drosophila* insulin-like genes provides a superior approach for identifying factors that are upstream of the receptor
20 in the signal transduction pathway. Specifically, components involved in the synthesis, activation and turnover of insulin-like proteins may be identified. Furthermore, the discovery of multiple, different insulin-like hormones provides a rational approach to separate components involved in responses to different, specific environmental or regulatory signals. This is less technically feasible with manipulation of downstream
25 components of the pathway found in target tissues. Further, the diversity of different insulin-like hormones provides a means to identify potential new receptor and/or signal transduction systems for insulin superfamily hormones that are structurally different from those that have been characterized to date, in either vertebrates or invertebrates. Still further, use of *Drosophila* as a system for analyzing the function and regulation of
30 insulin-like genes has great advantages over approaches in other organisms due to the ability to rapidly carry out large-scale, systematic genetic screens as well as the ability to screen small molecules directly on whole organisms for possible therapeutic or pesticide use. Particularly, the *Drosophila* insulin-like genes described herein are significantly

closer in structure to vertebrate insulin hormones than the insulin-like proteins of *C. elegans*; therefore, the fruit fly *Drosophila* may serve as a better model for vertebrate insulin function and signaling than the nematode *C. elegans* due to this greater structural similarity. Moreover, the fruit fly *Drosophila* is clearly the preferred genetic model organism for dissecting the function of insulin-like proteins, and validating potential pesticide targets, with respect to other insect pest species.

Isolation Of *D. Melanogaster* Insulin-Like Genes

In specific embodiments, insulin-like nucleic acids of the invention comprise the cDNA sequences of SEQ ID NO:1, SEQ ID NO:3, or SEQ ID NO:5 or the coding regions thereof, or nucleic acids encoding an insulin-like protein (*e.g.*, a protein having the sequence of SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6). As used herein, a gene "corresponding" to a cDNA sequence shall be construed to mean the gene that encodes the RNA from which the cDNA is derived. The invention provides purified or isolated nucleic acids consisting of at least 8 nucleotides (*i.e.*, a hybridizable portion) of an insulin-like gene sequence; in other embodiments, the nucleic acids consist of at least 25 (continuous) nucleotides, 50 nucleotides, 100 nucleotides, 150 nucleotides, or 200 nucleotides of an insulin-like sequence, or a full-length insulin-like coding sequence. In another embodiment, the nucleic acids are smaller than 35, 200, or 500 nucleotides in length. Nucleic acids can be single or double stranded. The invention also relates to nucleic acids hybridizable to or complementary to the foregoing sequences or their reverse complements. In specific aspects, nucleic acids are provided which comprise a sequence complementary to at least 10, 25, 50, 100, or 200 nucleotides or the entire coding region of an insulin-like gene.

The invention further relates to the genomic nucleotide sequences of *D. melanogaster* insulin-like nucleic acids. In specific embodiments, insulin-like nucleic acids comprise the genomic sequences of SEQ ID NO:7 or the coding regions thereof, or nucleic acids encoding an insulin-like protein (*e.g.*, a protein having the sequence of SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6).

In the above or alternative embodiments, the nucleic acids of the invention consist of a nucleotide sequence of not more than 2, 5, 10, 15, or 20 kilobases.

Hybridization Conditions

A nucleic acid which is hybridizable to an insulin-like nucleic acid (*e.g.*, having a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, or SEQ ID NO:5, or to its reverse complement, or to a nucleic acid encoding an insulin-like derivative, or to its reverse complement), under conditions of high, medium, or low stringency is provided. Methods
5 for selection of appropriate conditions for such stringencies is well known in the art (*see e.g.*, Sambrook et al., 1989, *supra*; Ausubel et al., eds., in the Current Protocols in Molecular Biology series of laboratory technique manuals, 8 1987-1997, Current Protocols, 8 1994-1997 John Wiley and Sons, Inc.).

An example of suitable conditions of high stringency that can be used is as follows.

10 Prehybridization of filters containing DNA is carried out for 8 h to overnight at 65°C in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 g/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65°C in prehybridization mixture containing 100 g/ml denatured salmon sperm DNA and 5-20 X 10⁶ cpm of ³²P-labeled probe. Washing of filters is done at 37°C for 1 h
15 in a solution containing 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA. This is followed by a wash in 0.1X SSC at 50°C for 45 min before autoradiography.

An example of procedures using conditions of medium stringency is as follows.

Filters containing DNA are pretreated for 6 h at 40°C in a solution containing 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.1% PVP, 0.1% Ficoll,
20 1% BSA, and 500 g/ml denatured salmon sperm DNA. Hybridizations are carried out in the same solution with the following modifications: 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 g/ml salmon sperm DNA, 10% (wt/vol) dextran sulfate, and 5-20 X 10⁶ cpm ³²P-labeled probe is used. Filters are incubated in hybridization mixture for 18-20 h at 40°C, and then washed for 1.5 h at 55°C in a solution containing 2X SSC, 25 mM
25 Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS. The wash solution is replaced with fresh solution and incubated an additional 1.5 h at 60°C. Filters are blotted dry and exposed for autoradiography. If necessary, filters are washed for a third time at 65-68°C and re-exposed to film.

Conditions of low stringency are as follows. Incubation for 8 hours to overnight at
30 37°C in a solution comprising 20% formamide, 5x SSC, 50mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA; hybridization in the same buffer for 18 to 20 hours; and washing of filters in 1x SSC at 37°C for 1 hour.

Fragments of insulin-like nucleic acids comprising regions conserved between (*i.e.*, with homology to) other insulin-like nucleic acids, of the same or different species, are also provided. Nucleic acids encoding one or more insulin-like domains are provided.

5 **Cloning Procedures**

The insulin-like genes of the invention can be cloned using any suitable technique known in the art (*see* Sambrook *et al.* (1989), *supra*; DNA Cloning: A Practical Approach, Vol. 1, 2, 3, 4, (1995) Glover, ed., MRL Press, Ltd., Oxford, U.K.). For example, with expression cloning, an expression library is constructed, mRNA is isolated, and cDNA is
10 made and ligated into an expression vector (*e.g.*, a bacteriophage derivative) that it is capable of being expressed by the host cell into which it is then introduced. Various screening assays can then be used to select for the expressed insulin-like product such as immunoassays using anti-insulin-like antibodies.

Polymerase chain reaction (PCR) can be used to amplify the desired sequence in a
15 genomic or cDNA library, prior to selection. Oligonucleotide primers representing known insulin-like sequences can be used as primers in PCR. Preferably, the oligonucleotide primers represent at least part of conserved segments of strong homology between insulin-like genes of different species. The synthetic oligonucleotides may be utilized as primers to amplify sequences from a source (RNA or DNA), preferably a cDNA library, of
20 potential interest. PCR can be carried out, *e.g.*, by use of a Perkin-Elmer Cetus thermal cycler and Taq polymerase (*e.g.*, Gene AmpJ). The nucleic acid being amplified can include mRNA or cDNA or genomic DNA from any species. One may synthesize degenerate primers for amplifying homologs from other species in the PCR reactions. The stringency of hybridization conditions used in priming the PCR reactions can be varied to
25 allow for greater or lesser degrees of nucleotide sequence similarity between the known insulin-like nucleotide sequences and a nucleic acid homolog (or ortholog) being isolated. For cross species hybridization, low stringency conditions are preferred. For same species hybridization, moderately stringent conditions are preferred. After successful amplification of a segment of an insulin-like homolog, that segment may be cloned and
30 sequenced by standard techniques, and utilized as a probe to isolate a complete cDNA or genomic clone. This, in turn, permits the determination of the gene's complete nucleotide sequence, the analysis of its expression, and the production of its protein product for functional analysis, as described below. In this fashion, additional genes encoding

insulin-like proteins and insulin-like analogs may be identified.

In another embodiment, the organizational characteristics of the insulin-like genes may be used to identify clones containing novel members of the insulin-like gene superfamily. For example, the insulin-like genes in the silkworm insect *B. Mori* (which
5 encode the bombyxin proteins) have been demonstrated to be organized in large multi gene clusters (Kondo, et al., 1996, J. Mol. Biol. 259:926-937). Identification and characterization of the genomic region surrounding a known insulin-like gene could, therefore, be used to identify additional genes that encode insulin-like proteins or insulin-like analogs that are located within these clusters by methods known in the art.

Any eukaryotic cell potentially can serve as the nucleic acid source for molecular cloning of an insulin-like gene. The nucleic acid sequences encoding insulin-like proteins may be isolated from vertebrate, mammalian, human, porcine, bovine, feline, avian, equine, canine, as well as additional primate sources, insects (*e.g., Drosophila*), invertebrates, plants, *etc.* The DNA may be obtained by standard procedures known in the
10 art from cloned DNA (*e.g., a DNA "library"*), by chemical synthesis, by cDNA cloning, or by the cloning of genomic DNA, or fragments thereof, purified from the desired cell.

In the molecular cloning of the gene from genomic DNA, DNA fragments are generated, some of which will encode the desired gene. The DNA may be cleaved at specific sites using various restriction enzymes. Alternatively, one may use DNase in the
20 presence of manganese to fragment the DNA, or the DNA can be physically sheared, as for example, by sonication. The linear DNA fragments can then be separated according to size by standard techniques such as agarose and polyacrylamide gel electrophoresis and column chromatography.

Once the DNA fragments are generated, identification of the specific DNA
25 fragment containing the desired gene may be accomplished in a number of ways. For example, if a portion of an insulin-like gene or its specific RNA or a fragment thereof is available and can be purified and labeled, the generated DNA fragments may be screened by nucleic acid hybridization to the labeled probe (Benton and Davis, 1977, Science 196:180; Grunstein and Hogness, 1975, Proc. Natl. Acad. Sci. U.S.A. 72:3961). Those
30 DNA fragments with substantial homology to the probe will hybridize. It is also possible to identify the appropriate fragment by restriction enzyme digestion(s) and comparison of fragment sizes with those expected according to a known restriction map if such is available. Further selection can be carried out on the basis of the properties of the gene.

Alternatively, the presence of the desired gene may be detected by assays based on the physical, chemical, or immunological properties of its expressed product. For example, cDNA clones, or DNA clones which hybrid-select the proper mRNAs, can be selected and expressed to produce a protein that has, *e.g.*, similar or identical

5 electrophoretic migration, isoelectric focusing behavior, proteolytic digestion maps, hormonal activity, binding activity, or antigenic properties as known for an insulin-like protein. Using an antibody to a known insulin-like protein, other insulin-like proteins may be identified by binding of the labeled antibody to expressed putative insulin-like proteins, *e.g.*, in an ELISA (enzyme-linked immunosorbent assay)-type procedure. Further, using a
10 binding protein specific to a known insulin-like protein, other insulin-like proteins may be identified by binding to such a protein (*see e.g.*, Clemmons, 1993, Mol. Reprod. Dev. 35:368-374; Loddick et al., 1998, Proc. Natl. Acad. Sci. U.S.A. 95:1894-1898).

An insulin-like gene can also be identified by mRNA selection using nucleic acid hybridization followed by *in vitro* translation. In this procedure, fragments are used to
15 isolate complementary mRNAs by hybridization. Such DNA fragments may represent available, purified insulin-like DNA of another species (*e.g.*, *Drosophila*, mouse, human).

Immunoprecipitation analysis or functional assays (*e.g.*, aggregation ability *in vitro*, binding to receptor, *etc.*) of the *in vitro* translation products of the isolated products of the isolated mRNAs identifies the mRNA and, therefore, the complementary DNA fragments
20 that contain the desired sequences. In addition, specific mRNAs may be selected by adsorption of polysomes isolated from cells to immobilized antibodies specifically directed against insulin-like protein. A radiolabeled insulin-like cDNA can be synthesized using the selected mRNA (from the adsorbed polysomes) as a template. The radiolabeled mRNA or cDNA may then be used as a probe to identify the insulin-like DNA fragments
25 from among other genomic DNA fragments.

Alternatives to isolating the insulin-like genomic DNA include, chemically synthesizing the gene sequence itself from a known sequence or making cDNA to the mRNA which encodes the insulin-like protein. For example, RNA for cDNA cloning of the insulin-like gene can be isolated from cells which express the gene.

30 The identified and isolated gene can then be inserted into an appropriate cloning vector. A large number of vector-host systems known in the art may be used. Possible vectors include, plasmids or modified viruses, but the vector system must be compatible with the host cell used. Suitable vectors include bacteriophages such as lambda

derivatives, or plasmids such as PBR322 or pUC plasmid derivatives or the Bluescript vector (Stratagene USA, La Jolla, California). The insertion into a cloning vector can, for example, be accomplished by ligating the DNA fragment into a cloning vector which has complementary cohesive termini. However, if the complementary restriction sites used to
5 fragment the DNA are not present in the cloning vector, the ends of the DNA molecules may be enzymatically modified. Alternatively, any site desired may be produced by ligating nucleotide sequences (linkers) onto the DNA termini; these ligated linkers may comprise specific chemically synthesized oligonucleotides encoding restriction endonuclease recognition sequences. In an alternative method, the cleaved vector and an
10 insulin-like gene may be modified by homopolymeric tailing. Recombinant molecules can be introduced into host cells via transformation, transfection, infection, electroporation, *etc.*, so that many copies of the gene sequence are generated.

In an alternative method, the desired gene may be identified and isolated after insertion into a suitable cloning vector in a "shot gun" approach. Enrichment for the
15 desired gene, for example, by size fractionization, can be done before insertion into the cloning vector.

In an additional embodiment, the desired gene may be identified and isolated after insertion into a suitable cloning vector using a strategy that combines a "shot gun" approach with a "directed sequencing" approach. Here, for example, the entire DNA
20 sequence of a specific region of the genome, such as a sequence tagged site (STS), can be obtained using clones that molecularly map in and around the region of interest.

In specific embodiments, transformation of host cells with recombinant DNA molecules that incorporate an isolated insulin-like gene, cDNA, or synthesized DNA sequence enables generation of multiple copies of the gene. Thus, the gene may be
25 obtained in large quantities by growing transformants, isolating the recombinant DNA molecules from the transformants and, when necessary, retrieving the inserted gene from the isolated recombinant DNA.

The insulin-like sequences provided by the instant invention include those nucleotide sequences encoding substantially the same amino acid sequences as found in
30 native insulin-like proteins. and those encoded amino acid sequences with functionally equivalent amino acids, as well as those encoding other insulin-like derivatives or analogs, as described below for insulin-like derivatives and analogs.

Expression Of *D. Melanogaster* Insulin-Like Genes

The nucleotide sequence coding for an insulin-like protein or a functionally active analog or fragment or other derivative thereof, can be inserted into any appropriate expression vector that contains the necessary elements for the transcription and translation of the inserted protein-coding sequence. The necessary transcriptional and translational signals can also be supplied by the native insulin-like gene and/or its flanking regions. A variety of host-vector systems may be utilized to express the protein-coding sequence such as mammalian cell systems infected with virus (*e.g.*, vaccinia virus, adenovirus, *etc.*); insect cell systems infected with virus (*e.g.*, baculovirus); microorganisms such as yeast containing yeast vectors, or bacteria transformed with bacteriophage, DNA, plasmid DNA, or cosmid DNA. The expression elements of vectors vary in their strengths and specificities. Depending on the host-vector system utilized, any one of a number of suitable transcription and translation elements may be used. In yet another embodiment, a fragment of an insulin-like protein comprising one or more domains of the insulin-like protein is expressed.

Any of the methods previously described for the insertion of DNA fragments into a vector may be used to construct expression vectors containing a chimeric gene consisting of appropriate transcriptional/translational control signals and the protein coding sequences. These methods may include *in vitro* recombinant DNA and synthetic techniques and *in vivo* recombinants (genetic recombination). Expression of a nucleic acid sequence encoding an insulin-like protein or peptide fragment may be regulated by a second nucleic acid sequence so that the insulin-like protein or peptide is expressed in a host transformed with the recombinant DNA molecule. For example, expression of an insulin-like protein may be controlled by any promoter/enhancer element known in the art including those of prokaryotic expression vectors and plant expression vectors; promoter elements from yeast or other fungi; and transcriptional control regions. In some embodiments, the promoter will exhibit tissue specificity. In a specific embodiment, a vector is used that comprises a promoter operably linked to an insulin-like gene nucleic acid, one or more origins of replication, and, optionally, one or more selectable markers (*e.g.*, an antibiotic resistance gene).

Expression constructs can be made by subcloning an insulin-like coding sequence into the EcoRI restriction site of each of the three pGEX vectors (Smith and Johnson, 1988, Gene 7:31-40). This allows for the expression of the insulin-like protein

product from the subclone in the correct reading frame. Expression vectors containing insulin-like gene inserts can be identified by three general approaches: (a) nucleic acid hybridization; (b) presence or absence of "marker" gene functions; and (c) expression of inserted sequences. In the first approach, the presence of an insulin-like gene inserted in an expression vector can be detected by nucleic acid hybridization using probes
5 comprising sequences that are homologous to an inserted insulin-like gene. In the second approach, the recombinant vector/host system can be identified and selected based upon the presence or absence of certain "marker" gene functions (*e.g.*, thymidine kinase activity, resistance to antibiotics, transformation phenotype, occlusion body
10 formation in baculovirus, *etc.*) caused by the insertion of an insulin-like gene in the vector. For example, if the insulin-like gene is inserted within the marker gene sequence of the vector, recombinants containing the insulin-like insert can be identified by the absence of the marker gene function. In the third approach, recombinant expression vectors can be identified by assaying the insulin-like product expressed by
15 the recombinant. Such assays can be based, for example, on the physical or functional properties of the insulin-like protein in *in vitro* assay systems, *e.g.*, binding with anti-insulin-like protein antibody.

Once a particular recombinant DNA molecule is identified and isolated, several methods known in the art may be used to propagate it. Once a suitable host system and
20 growth conditions are established, recombinant expression vectors can be propagated and prepared in quantity. Some of the expression vectors which can be used include human or animal viruses such as vaccinia virus or adenovirus; insect viruses such as baculovirus; yeast vectors; bacteriophage vectors (*e.g.*, lambda phage), and plasmid and cosmid DNA vectors.

25 In addition, a host cell strain may be chosen that modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Expression from certain promoters can be elevated in the presence of certain inducers; thus, expression of the genetically engineered insulin-like protein may be controlled. Furthermore, different host cells have characteristic and specific
30 mechanisms for the translational and post-translational processing and modification (*e.g.*, glycosylation, phosphorylation of proteins. Appropriate cell lines or host systems can be chosen to ensure the desired modification and processing of the foreign protein expressed. For example, expression in a bacterial system can be used to produce a non-

glycosylated core protein product. Expression in yeast will produce a glycosylated product. Expression in mammalian cells can be used to ensure "native" glycosylation of a heterologous protein. Furthermore, different vector/host expression systems may effect processing reactions to different extents.

5 In other embodiments of the invention, the insulin-like protein, fragment, analog, or derivative may be expressed as a fusion, or chimeric protein product (comprising the protein, fragment, analog, or derivative joined via a peptide bond to a heterologous protein sequence of a different protein). Such a chimeric product can be made by ligating the appropriate nucleic acid sequences encoding the desired amino
10 acid sequences to each other by methods known in the art, in the proper coding frame, and expressing the chimeric product by methods commonly known in the art. Alternatively, such a chimeric product may be made by protein synthetic techniques, *e.g.*, by use of a peptide synthesizer.

15 **Identification And Purification Of Gene Products**

In particular aspects, the invention provides amino acid sequences of insulin-like proteins and fragments and derivatives thereof which comprise an antigenic determinant (*i.e.*, can be recognized by an antibody) or which are otherwise functionally active, as well as nucleic acid sequences encoding the foregoing. "Functionally active" insulin-like
20 material as used herein refers to that material displaying one or more functional activities associated with a full-length (wild-type) insulin-like protein, *e.g.*, binding to an insulin-like receptor (*e.g.*, InR or insulin-like protein binding partner, antigenicity (binding to an anti- insulin-like protein antibody), immunogenicity, *etc.*

In specific embodiments, the invention provides fragments of an insulin-like
25 protein consisting of at least 10 amino acids, 20 amino acids, 50 amino acids, or of at least 75 amino acids. In other embodiments, the proteins comprise or consist essentially of an insulin-like B peptide domain, an insulin-like A peptide domain, an insulin-like C peptide domain, or any combination of the foregoing, of an insulin-like protein. Fragments, or proteins comprising fragments, lacking some or all of the foregoing regions of a
30 insulin-like protein are also provided. Nucleic acids encoding the foregoing are provided. In specific embodiments, the foregoing proteins or fragments are not more than 25, 50, or 100 contiguous amino acids.

Once a recombinant which expresses the insulin-like gene sequence is identified,

the gene product can be analyzed. This is achieved by assays based on the physical or functional properties of the product, including radioactive labeling of the product followed by analysis by gel electrophoresis, immunoassay, *etc.*

Once the insulin-like protein is identified, it may be isolated and purified by standard methods including chromatography (*e.g.*, ion exchange, affinity, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of proteins. The functional properties may be evaluated using any suitable assay.

Alternatively, once an insulin-like protein produced by a recombinant is identified, the amino acid sequence of the protein can be deduced from the nucleotide sequence of the chimeric gene contained in the recombinant. As a result, the protein can be synthesized by standard chemical methods known in the art (*e.g.*, *see* Hunkapiller et al., 1984, *Nature* 310:105-111).

In another alternate embodiment, native insulin-like proteins can be purified from natural sources, by standard methods such as those described above (*e.g.*, immunoaffinity purification).

In a specific embodiment of the present invention, such insulin-like proteins, whether produced by recombinant DNA techniques or by chemical synthetic methods or by purification of native proteins, include but are not limited to those containing, as a primary amino acid sequence, all or part of the amino acid sequence substantially as depicted in Figs. 5-7 (SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6, respectively), as well as fragments and other derivatives, and analogs thereof, including proteins homologous thereto.

Structure Of Insulin-Like Genes And Proteins

The structure of insulin-like genes and proteins of the invention can be analyzed by various methods known in the art, including genetic analysis and protein analysis.

Genetic analysis methods for determining the structure of cloned DNA or cDNA corresponding to an insulin-like include Southern hybridization, Northern hybridization, restriction endonuclease mapping, and DNA sequence analysis. Accordingly, this invention provides nucleic acid probes recognizing an insulin-like gene. For example, polymerase chain reaction followed by Southern hybridization with an insulin-like gene-specific probe can allow the detection of an insulin-like gene in DNA from various

cell types. Methods of amplification other than PCR are commonly known and can also be employed. In one embodiment, Southern hybridization can be used to determine the genetic linkage of an insulin-like gene. Northern hybridization analysis can be used to determine the expression of an insulin-like gene. Various cell types, at various states of development or activity can be tested for insulin-like gene expression. The stringency of the hybridization conditions for both Southern and Northern hybridization can be manipulated to ensure detection of nucleic acids with the desired degree of relatedness to the specific insulin-like gene probe used. Modifications of these methods and other methods commonly known in the art can be used.

Restriction endonuclease mapping can be used to roughly determine the genetic structure of an insulin-like gene. Restriction maps derived by restriction endonuclease cleavage can be confirmed by DNA sequence analysis.

DNA sequence analysis can be performed by any techniques known in the art, such as the method of Maxam and Gilbert (1980, Meth. Enzymol. 65:499-560), the Sanger dideoxy method (Sanger et al., 1977, Proc. Natl. Acad. Sci. U.S.A. 74:5463), the use of T7 DNA polymerase (Tabor and Richardson, U.S. Patent No. 4,795,699), or use of an automated DNA sequenator (*e.g.*, Applied Biosystems, Foster City, California).

The amino acid sequence of an insulin-like protein can be derived by deduction from the DNA sequence, or alternatively, by direct sequencing of the protein, *e.g.*, with an automated amino acid sequencer. An insulin-like protein sequence can be further characterized by a hydrophilicity analysis (Hopp and Woods, 1981, Proc. Natl. Acad. Sci. U.S.A. 78:3824). A hydrophilicity profile can be used to identify the hydrophobic and hydrophilic regions of the insulin-like protein and the corresponding regions of the gene sequence that encode such regions.

Secondary, structural analysis (Chou and Fasman, 1974, Biochemistry 13:222) can also be done, to identify regions of an insulin-like protein that assume specific secondary structures.

Manipulation, translation, and secondary structure prediction, open reading frame prediction and plotting, as well as determination of sequence homologies, can also be accomplished using computer software programs available in the art.

Other methods of structural analysis include X-ray crystallography, nuclear magnetic resonance spectroscopy and computer modeling.

Antibodies

The insulin-like protein of SEQ ID NOs:2, 4 and 6, or fragments or derivatives thereof, may be used as an immunogen to generate antibodies. Such antibodies include polyclonal, monoclonal, chimeric, single chain, Fab fragments, and an Fab expression
5 library. In another embodiment, antibodies to a domain (*e.g.*, an insulin-like receptor binding domain) of an insulin-like protein are produced. In a specific embodiment, fragments of an insulin-like protein identified as hydrophilic are used as immunogens for antibody production using art-known methods. Some examples of suitable techniques include methods which provides for the production of antibody molecules by continuous
10 cell lines in culture; the production of monoclonal antibodies in germ-free animals (*see e.g.*, PCT/US90/02545); the use of human hybridomas (Cole et al., 1983, Proc. Natl. Acad. Sci. U.S.A. 80:2026-2030); transforming human B cells with EBV virus *in vitro* (Cole et al., 1985, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, pp. 77-96). Additionally, known techniques can be used for the production of "chimeric antibodies"
15 (*e.g.* by splicing the genes from a mouse antibody molecule specific for an insulin-like protein together with genes from a human antibody molecule of appropriate biological activity), insulin-like-specific single chain antibodies; and Fab expression libraries (*e.g.* to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity for insulin-like proteins, derivatives, or analogs). The foregoing antibodies can
20 be used against the insulin-like protein sequences described herein, *e.g.*, for imaging these proteins, measuring levels thereof, in diagnostic methods, *etc.*

Insulin-Like Proteins, Derivatives And Analogs

The invention relates to insulin-like proteins and derivatives, fragments, and
25 analogs thereof, as well as the nucleic acids encoding them. In one embodiment, the insulin-like proteins are encoded by the insulin-like nucleic acids described above. In particular aspects, the proteins, derivatives, or analogs are of insulin-like proteins encoded by the sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, or SEQ ID NO:7.

In a specific embodiment, the insulin-like protein fragment, derivative or analog is
30 functionally active, *i.e.*, capable of exhibiting one or more functional activities associated with a full-length, wild-type insulin-like protein. As one example, such fragments, derivatives or analogs have the desired immunogenicity or antigenicity for use in immunoassays, for immunization, for inhibition of insulin-like activity, *etc.* As another

example, such fragments, derivatives or analogs which have the desired binding activity can be used for binding to the InR gene product. As yet another example, they have the desired binding activity can be used for binding to a binding protein specific for a known insulin-like protein (*see e.g.*, Clemmons, 1993, Mol. Reprod. Dev. 35:368-374; Loddick et al., 1998, Proc. Natl. Acad. Sci. U.S.A. 95:1894-1898). Derivatives or analogs that retain, or alternatively lack or inhibit, a desired insulin-like protein property-of-interest (*e.g.*, binding to an insulin-like protein binding partner), can be used as inducers, or inhibitors, respectively, of such property and its physiological correlates. A specific embodiment relates to an insulin-like protein fragment that can be bound by an anti-insulin-like protein antibody. Derivatives or analogs of an insulin-like protein can be tested for the desired activity by procedures known in the art.

In particular, insulin-like derivatives can be made by altering insulin-like sequences by substitutions, additions (*e.g.*, insertions) or deletions that provide for functionally equivalent molecules. Due to the degeneracy of nucleotide coding sequences, other DNA sequences which encode substantially the same amino acid sequence as an insulin-like gene may be used in the practice of the present invention. These include nucleotide sequences comprising all or portions of an insulin-like gene which is altered by the substitution of different codons that encode a functionally equivalent amino acid residue within the sequence, thus producing a silent change. Likewise, the insulin-like derivatives of the invention include those containing, as a primary amino acid sequence, all or part of the amino acid sequence of an insulin-like protein including altered sequences in which functionally equivalent amino acid residues are substituted for residues within the sequence resulting in a silent change. For example, one or more amino acid residues within the sequence can be substituted by another amino acid of a similar polarity which acts as a functional equivalent, resulting in a silent alteration. Substitutions for an amino acid within the sequence may be selected from other members of the class to which the amino acid belongs. For example, the nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine. The polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine. The positively charged (basic) amino acids include arginine, lysine and histidine. The negatively charged (acidic) amino acids include aspartic acid and glutamic acid. Such substitutions are generally understood to be conservative substitutions.

In a specific embodiment of the invention, proteins consisting of or comprising a fragment of an insulin-like protein of at least 10 (continuous) amino acids of the insulin-like protein is provided. In other embodiments, the fragment comprises at least 20, 50, or 75 amino acids of the insulin-like protein. In specific embodiments, such fragments are not larger than 35, 100 or 200 amino acids. Derivatives or analogs of insulin-like proteins may comprise regions that are substantially homologous to an insulin-like protein or fragment thereof (*e.g.*, in various embodiments, at least 60% or 70% or 80% or 90% or 95% identity over an amino acid sequence of identical size. As used herein, "percent (%) sequence identity" with respect to a subject sequence, or a specified portion of a subject sequence, is defined as the percentage of nucleotides or amino acids in the candidate sequence identical with the nucleotides in the subject sequence (or specified portion thereof), after aligning the sequences and introducing gaps, if necessary to achieve the maximum percent sequence identity, as generated by the program WU-BLAST-2.0a19 (Altschul *et al.*, J. Mol. Biol. (1997) 215:403-410; <http://blast.wustl.edu/blast/README.html>; (hereinafter referred to generally as "BLAST") with all the search parameters set to default values. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched. A percent (%) identity value is determined by the number of matching identical nucleotides or amino acids divided by the sequence length for which the percent identity is being reported.

The insulin-like derivatives and analogs of the invention can be produced by various methods known in the art. The manipulations which result in their production can occur at the gene or protein level. For example, a cloned insulin-like gene sequence can be modified by any of numerous strategies known in the art (Sambrook *et al.*, 1989). The sequence can be cleaved at appropriate sites with restriction endonuclease(s), followed by further enzymatic modification if desired, isolated, and ligated *in vitro*. Additionally, an insulin-like nucleic acid sequence can be mutated *in vitro* or *in vivo*, to create and/or destroy translation, initiation, and/or termination sequences, or to create variations in coding regions and/or to form new restriction endonuclease sites or destroy preexisting ones, to facilitate further *in vitro* modification. Any technique for mutagenesis known in the art can be used, for example, chemical mutagenesis, *in vitro* site-directed mutagenesis (Hutchinson *et al.*, 1978, J. Biol. Chem. 253:6551), use of TAB7 linkers (Pharmacia),

PCR with primers containing a mutation, *etc.*

Manipulations of an insulin-like protein sequence may also be made at the protein level. Included within the scope of the invention are insulin-like protein fragments or other derivatives or analogs which are differentially modified during or after translation, *e.g.*, by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, *etc.* Any of numerous chemical modifications may be carried out by known techniques, such as specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, NaBH₄, acetylation, formylation, oxidation, reduction, metabolic synthesis in the presence of tunicamycin, *etc.*

In addition, analogs and derivatives of an insulin-like protein can be chemically synthesized. For example, a peptide corresponding to a portion of an insulin-like protein which comprises the desired domain, or which mediates the desired activity *in vitro*, can be synthesized by use of a peptide synthesizer. Furthermore, if desired, nonclassical amino acids or chemical amino acid analogs can be introduced as a substitution or addition into the insulin-like sequence. Examples of non-classical amino acids include the D-isomers of the common amino acids, α -amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid, β -Abu, β -Ahx, 6-amino hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine, norvaline, hydroxyproline, sarcosine, citrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, β -alanine, fluoro-amino acids, designer amino acids such as α -methyl amino acids, C-methyl amino acids, N-methyl amino acids, and amino acid analogs in general. Furthermore, the amino acid can be D (dextrorotary) or L (levorotary).

In a specific embodiment, an insulin-like protein derivative is a chimeric or fusion protein comprising an insulin-like protein or fragment thereof (preferably consisting of at least a domain or motif of the insulin-like protein, or at least 10 amino acids of the insulin-like protein) joined at its amino- or carboxy-terminus via a peptide bond to an amino acid sequence of a different protein. In specific embodiments, the amino acid sequence of the different protein is at least 6, 10, 20 or 30 continuous amino acids of the different proteins or a portion of the different protein that is functionally active. In one embodiment, such a chimeric protein is produced by recombinant expression of a nucleic acid encoding the protein (comprising an insulin-like-coding sequence joined in-frame to a coding sequence for a different protein). Such a chimeric product can be made by ligating

the appropriate nucleic acid sequences encoding the desired amino acid sequences to each other by methods known in the art, in the proper coding frame, and expressing the chimeric product by methods commonly known in the art. Alternatively, such a chimeric product may be made by protein synthetic techniques, *e.g.*, by use of a peptide synthesizer.

5 Chimeric genes comprising portions of an insulin-like gene fused to any heterologous protein-encoding sequences may be constructed. A specific embodiment relates to a chimeric protein comprising a fragment of an insulin-like protein of at least six amino acids, or a fragment that displays one or more functional activities of the insulin-like protein.

10 In another specific embodiment, the insulin-like derivative is a molecule comprising a region of homology with a insulin-like protein. By way of example, in various embodiments, a first protein region can be considered "homologous" to a second protein region when the amino acid sequence of the first region is at least 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, or 95% identical, when compared to any sequence in
15 the second region of an equal number of amino acids as the number contained in the first region or when compared to an aligned sequence of the second region that has been aligned by a computer homology program known in the art. For example, a molecule can comprise one or more regions homologous to an insulin-like domain or a portion thereof.

In a specific embodiment, the invention relates to insulin-like derivatives and
20 analogs, in particular insulin-like fragments and derivatives of such fragments, that comprise, or alternatively consist of, one or more domains of an insulin-like protein, including but not limited to an insulin-like B peptide domain, an insulin-like A peptide domain, or an insulin-like connecting (C) peptide domain.

A specific embodiment relates to molecules comprising specific fragments of an
25 insulin-like protein that are those fragments in the respective insulin-like proteins of the invention most homologous to specific fragments of a human or mouse insulin-like protein. A fragment comprising a domain of an insulin-like homolog can be identified by protein analysis methods well known in the art. In another specific embodiment, a molecule is provided that comprises one or more domains (or functional portion thereof)
30 of an insulin-like protein. In particular examples, insulin-like protein derivatives are provided that contain either an A peptide domain or a B peptide domain. By way of another example, such a protein may retain such domains separated by a peptide spacer. Such spacer may be the same as or different from an insulin-like connecting (C) peptide.

In another embodiment, a molecule is provided that comprises one or more domains (or functional portion(s) thereof) of an insulin-like protein, and that has one or more mutant (e.g., due to deletion or point mutation(s)) domains of an insulin-like protein (e.g., such that the mutant domain has decreased function).

5

Generation And Genetic Analysis Of *Drosophila* With Altered Insulin-Like Genes

The present invention provides for methods of creating genetically-engineered fruit flies and laboratory-generated mutant fruit flies.

Genetically-engineered fruit flies can be made that harbor one or more deletions or
10 insertions in an insulin-like gene or genes. In another embodiment, genetically-engineered fruit flies harbor interfering RNAs derived from such genes. In another embodiment, genetically-engineered fruit flies harbor one or more transgenes for mis-expression of wild-type or mutant forms of such genes. Mutant fruit flies can be generated in the lab to contain deletions, insertions, rearrangements, or point mutations in an insulin-like gene or
15 genes, or combinations thereof.

The present invention provides a method by which *Drosophila* strains with laboratory-generated alterations in insulin-like genes may be used for the identification of insulin-like genes that participate in particular biochemical and/or genetic pathways. In a specific embodiment, *Drosophila* strains with laboratory-generated alterations in one or
20 more insulin-like genes may be used for the identification of insulin-like genes that participate in biochemical and/or genetic pathways that constitute possible pesticide targets, as judged by phenotypes such as non-viability, block of normal development, defective feeding, defective movement, or defective reproduction. That is, development of such a phenotype in a *Drosophila* containing an alteration in a *Drosophila* insulin-like
25 gene indicates that the insulin-like gene is a potential pesticide target.

In another embodiment, *Drosophila* strains with laboratory-generated alterations relate to therapeutic applications associated with the insulin superfamily hormones, such as metabolic control, growth regulation, differentiation, reproduction, and aging.

In another embodiment, *Drosophila* strains with laboratory-generated alterations
30 relate to large-scale genetic modifier screens aimed at systematic identification of components of genetic and/or biochemical pathways that serve as novel drug targets, diagnostics, prognostics, therapeutic proteins, pesticide targets or protein pesticides.

The invention provides methods for creating and analyzing *Drosophila* strains

having modified expression of insulin-like genes, as described below. In one embodiment, expression modification methods include any method known to one skilled in the art. Specific examples include chemical mutagenesis, transposon mutagenesis, antisense RNA interference, and transgene-mediated mis-expression. In the creation of transgenic
5 animals, it is preferred that heterologous (*i.e.*, non- native) promoters be used to drive transgene expression.

Generation Of Loss-Of-Function Mutation In Insulin-Like Gene

The present invention provides methods of testing for preexisting mutations in a *D.*
10 *melanogaster* insulin-like gene. In a specific embodiment, the genomic sequence containing the entire insulin cluster can be used to determine whether an existing mutant *Drosophila* line corresponds to a mutation in one or more of the insulin-like genes. Mutations in genes that map to the same genetic region as the insulin-like gene cluster (chromosomal band 67C-D) are of particular interest. For example, a large number of
15 previously identified mutations have been mapped to the approximate genetic region of the insulin cluster (67C-D), including l(3)67BDa, l(3)67BDb, l(3)67BDc, l(3)67BDd, l(3)67BDe, l(3)67BDf, l(3)67BDg l(3)67BDh, l(3)67BDi l(3)67BDj, l(3)67BDk, l(3)67BDl, l(3)67BDM, l(3)67BDn, l(3)67BDp, l(3)67BDq, l(3)67BDr (FlyBase: a *Drosophila* database, Flybase consortium, Harvard University); however, the normal
20 function of these genes has not been determined. To ascertain whether any of these mutations are in an insulin-like gene, a genomic fragment containing the *Drosophila* insulin gene cluster and potential flanking regulatory regions can be subcloned into any appropriate *Drosophila* transformation vector, such as the Carnegie series of vectors (Rubin and Spradling, 1983, Nucleic Acids Res. 11(18):6341-51), the pCaspeR series of
25 vectors (Thummel, et al., 1988, Gene 74(2):445-56), or the pW8 vector (Klemenz, et al., 1987, Nucleic Acids Res. 15(10):3947-59) and injected into flies along with an appropriate helper plasmid to supply transposase. Resulting transformants are crossed for complementation testing to an existing panel of *Drosophila* lines containing mutations that have been mapped to the appropriate genomic region (67C-D) as described above
30 (Greenspan, 1997, in *Fly pushing: The Theory and Practice of Drosophila Genetics* Cold Spring Harbor Press, Plainview, NY, pp. 3-46). If a mutant line is discovered to be rescued by this genomic fragment, as judged by complementation of the mutant phenotype, progressively smaller subclones or clones containing a single insulin gene can

be individually tested until the responsible locus is identified.

Generating Loss-Of-Function Mutations By Mutagenesis

Further, the invention herein provides a method for generating loss-of-function mutations in a *D. melanogaster* insulin-like gene. Mutations can be generated by one of many mutagenesis methods known to investigators skilled in the art (Ashburner, 1989, In *Drosophila: A Laboratory Manual*, Cold Spring Harbor, NY, Cold Spring Harbor Laboratory Press: pp. 299-418.; “*Fly pushing: The Theory and Practice of Drosophila Genetics*” Cold Spring Harbor Press, Plainview, NY). In a specific embodiment, the mutagens that can be used include but are not restricted to: transposons such as the P or hobo elements; chemical mutagens such as ethylmethane sulfonate (EMS), methylmethane sulfonate (MMS), N-ethyl-N-nitrosourea (ENU), triethylmelamine, diepoxyalkanes, ICR-170, or formaldehyde; and irradiation with X-rays, gamma rays, or ultraviolet radiation.

Mutagenesis by P elements, or marked P elements, is particularly appropriate for isolation of loss-of-function mutations in *Drosophila* insulin-like genes due to the precise molecular mapping of these genes, the small size of these targets, the availability and proximity of preexisting P element insertions for use as a localized transposon source, and the potential to knock out several of these genes by induction of a small deletion of the locus (Hamilton and Zinn, 1994, *Methods in Cell Biology* 44:81-94; Wolfner and Goldberg, 1994, *Methods in Cell Biology* 44:33-80; Clark, et al., 1994, *Proc. Natl. Acad. Sci. U.S.A.* 91(2):719-22; Kaiser, 1990, *Bioessays* 12(6):297-301, In *Drosophila melanogaster: Practical Uses in Cell and Molecular Biology*, L.S.B. Goldstein and E. A. Fyrberg, Eds., Academic Press, Inc. San Diego, California). For the purposes of mutagenesis, modified P elements are typically used which contain one or more of the following elements: sequences encoding a dominant visible marker, usually a wild-type *white+* or *rosy+* eye color gene, to allow detection of animals containing the P element and to screen for transposition events (Rubin and Spradling, 1982, *Science* 218(4570):348-53; Klemenz, et al., 1987, *Nucleic Acids Res.* 15(10):3947-59), bacterial plasmid sequences including a selectable marker such as ampicillin resistance to facilitate cloning of genomic sequences adjacent to the insertion site (Steller and Pirrotta, 1985, *Embo. J.* 4:167-171) and *lacZ* sequences fused to a weak general promoter to detect the presence of enhancers with a developmental expression pattern of interest (Bellen, et al., 1989, *Genes Dev.*

3(9):1288-300; Bier, et al., 1989, Genes Dev. 3(9):1273-87; Wilson, et al., 1989, Genes Dev. 3(9):1301-13). For examples of marked P elements useful for mutagenesis see "FlyBase - A Drosophila Database", Nucleic Acids Research 26:85-88, (<http://flybase.bio.indiana.edu>).

5 A preferred method of transposon mutagenesis employs the "local hopping" method (Tower et al., 1993, Genetics 133:347-359). Briefly, an existing mutant *Drosophila* line containing a P element inserted into chromosomal bands 67C-D, such as l(3)01859 or any other P element that maps within this region, is crossed to a *Drosophila* line expressing transposase in order to mobilize the transposon. Transposition of the P
10 element, which contains a marker gene that typically affects eye color, is determined phenotypically on the basis of eye color change in the resulting progeny. Candidate insertion lines are selected for further analysis on the basis of close linkage of the new insertion to the initial insertion site, which can be determined by standard genetic mapping techniques such as high frequency cosegregation of markers. Each new P insertion line
15 can be tested molecularly for transposition of the P element into the insulin-like gene cluster by assays based on PCR amplification. For each reaction, one PCR primer is used that is homologous to sequences contained within the P element and a second primer is homologous to one of the individual insulin genes, in either the coding region or flanking regions of the insulin-like gene. Products of the PCR reactions are detected by agarose gel
20 electrophoresis. The sizes of the resulting DNA fragments are used to map the site of P element insertion.

Alternatively, Southern blotting and restriction mapping using DNA probes derived from genomic DNA or cDNAs of the insulin-like genes can be used to detect transposition events that rearrange the genomic DNA of the insulin-like genes. P
25 transposition events that map to the insulin gene cluster can be assessed for phenotypic effects in heterozygous or homozygous mutant *Drosophila*, as described in detail below.

Generating Localized Deletions In The Insulin Gene Cluster

In another embodiment, *Drosophila* lines carrying P insertions in the insulin gene
30 cluster can be used to generate localized deletions in the insulin-like gene cluster by previously described methods known in the art (Kaiser, 1990, Bioessays 12(6):297-301; Harnessing the power of *Drosophila* genetics, In *Drosophila melanogaster: Practical Uses in Cell and Molecular Biology*, L.S.B. Goldstein and E. A. Fyrberb, eds., Academic Press,

Inc. San Diego, California). This is particularly useful if no P elements transpositions are found that disrupt a particular insulin-like gene of interest. In brief, flies containing P elements inserted into the insulin gene cluster are exposed to a further round of transposase to induce excision of the element. Progeny in which the transposon has excised are typically identified by loss of the eye color marker associated with the transposable element. The resulting progeny will include flies with either precise or imprecise excision of the P element, where the imprecise excision events often result in deletion of genomic DNA neighboring the site of P insertion. Such progeny can be screened by molecular techniques to identify deletion events that remove flanking genomic sequence. Such methods include, (a) methods of detecting alterations in the genomic DNA based on PCR amplification with primers flanking the insertion site of the P element; (b) methods based on Southern blotting and restriction mapping using DNA probes derived from the P element, DNA probes derived from flanking genomic sequence in the region of the insulin-like genes, or DNA probes derived from cDNAs of insulin-like genes. Deletions generated in this manner that remove one or more of the insulin-like loci can be assessed for phenotypic effects in heterozygous and homozygous mutant *Drosophila* as described below.

Generating Loss-Of-Function Phenotypes Using Methods Based On RNA-Mediated Interference With Gene Expression

The invention further provides a method for generating loss-of-function phenotypes using methods based on RNA-mediated interference with gene expression. The function of the *Drosophila* insulin-like genes identified herein may be characterized and/or determined by generating loss-of-function phenotypes through such RNA-based methods.

In one embodiment, loss-of-function phenotypes are generated by antisense RNA methods (Schubiger and Edgar, 1994, Methods in Cell Biology 44:697-713). One form of the antisense RNA method involves the injection of embryos with an antisense RNA that is partially homologous to the gene-of-interest (in this case an insulin-like gene). Another form of the antisense RNA method involves expression of an antisense RNA partially homologous to the gene-of-interest by operably joining a portion of the gene-of-interest in the antisense orientation to a powerful promoter that can drive the expression of large quantities of antisense RNA, either generally throughout the animal or in specific tissues.

Examples of powerful promoters that can be used in this strategy of antisense RNA include heat shock gene promoters or promoters controlled by potent exogenous transcription factors, such as GAL4 and tTA, described in more detail in the following section. Antisense RNA-generated loss-of-function phenotypes have been reported previously for several *Drosophila* genes including *cactus*, *pecanex*, and *Krupple* (LaBonne, et al., 1989, Dev. Biol. 136(1):1-16; Schuh and Jackle, 1989, Genome 31(1):422-5; Geisler, et al., 1992, Cell 71(4):613-21).

In a second embodiment, loss-of-function phenotypes are generated by cosuppression methods (Bingham, 1997, Cell 90(3):385-7; Smyth, 1997, Curr. Biol. 7(12):793-5; Que and Jorgensen, 1998, Dev. Genet. 22(1):100-9). Cosuppression is a phenomenon of reduced gene expression produced by expression or injection of a sense strand RNA corresponding to a partial segment of the gene-of-interest. Cosuppression effects have been employed extensively in plants to generate loss-of-function phenotypes, and there is report of cosuppression in *Drosophila* where reduced expression of the *Adh* gene was induced from a *white-Adh* transgene (Pal-Bhadra, et al., 1997, Cell 90(3):479-90).

In a third embodiment, loss-of-function phenotypes may be generated by double-stranded RNA interference. This method is based on the interfering properties of double-stranded RNA derived from the coding regions of genes. Termed dsRNAi, this method has proven to be of great utility in genetic studies of the nematode *C. elegans* (see Fire et al., 1998, Nature 391:806-811). In a preferred embodiment of this method, complementary sense and antisense RNAs derived from a substantial portion of a gene-of-interest, such as an insulin-like gene, are synthesized *in vitro*. Phagemid DNA templates containing cDNA clones of the gene-of-interest are inserted between opposing promoters for T3 and T7 phage RNA polymerases. Alternatively, one can use PCR products amplified from coding regions of insulin-like genes, where the primers used for the PCR reactions are modified by the addition of phage T3 and T7 promoters. The resulting sense and antisense RNAs are annealed in an injection buffer, and the double-stranded RNA injected or otherwise introduced into animals. Progeny of the injected animals are then inspected for phenotypes-of-interest.

ANTISENSE REGULATION OF GENE EXPRESSION

The invention provides for antisense uses of *D. melanogaster* insulin-like genes.

In a specific embodiment, an insulin-like protein function is inhibited by use of insulin-like antisense nucleic acids. The present invention provides for use of nucleic acids of at least six nucleotides that are antisense to a gene or cDNA encoding an insulin-like protein or a portion thereof. An insulin-like "antisense" nucleic acid as used
5 herein refers to a nucleic acid capable of hybridizing to a sequence-specific (i.e. non-poly A) portion of an insulin-like RNA (preferably mRNA) by virtue of some sequence complementarily. Antisense nucleic acids may also be referred to as inverse complement nucleic acids. The antisense nucleic acid may be complementary to a coding and/or noncoding region of an insulin-like mRNA. Such antisense nucleic acids have utility in
10 inhibiting an insulin-like protein function. For example, such antisense nucleic acids may be useful as pesticides to eradicate parasites in plants, or in animals such as dogs, horses, and cattle.

The antisense nucleic acids of the invention can be oligonucleotides that are double-stranded or single-stranded, RNA or DNA or a modification or derivative thereof,
15 which can be directly administered to a cell, or which can be produced intracellularly by transcription of exogenous introduced sequences. In a preferred embodiment, the antisense nucleic acids of the invention are double-stranded RNA mentioned previously (*see* Fire et al., 1998, Nature 391:806-811).

The insulin-like antisense nucleic acids of the invention are preferably
20 oligonucleotides (ranging from 6 to about 50 oligonucleotides). In specific aspects, an oligonucleotide is at least 10 nucleotides, at least 15 nucleotides, at least 100 nucleotides, or at least 200 nucleotides in length. The oligonucleotide can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof, or single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or
25 phosphate backbone. The oligonucleotide may include other appending groups such as peptides, or agents facilitating transport across the cell membrane (*see e.g.*, Letsinger et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. U.S.A. 84:648-652; PCT Publication No. WO 88/09810, published December 15, 1988) or the blood-brain barrier (*see e.g.*, PCT Publication No. WO 89/10134,
30 published April 25, 1988), hybridization-triggered cleavage agents (*see e.g.*, Krol et al., 1988, BioTechniques 6:958-976) or intercalating agents (*see e.g.*, Zon, 1988, Pharm. Res. 5:539-549).

In a preferred aspect of the invention, an insulin-like antisense oligonucleotide is

provided as single-stranded DNA. In another preferred aspect, such an oligonucleotide comprises a sequence antisense to the sequence encoding a B peptide domain or an A peptide domain of an insulin-like protein. The oligonucleotide may be modified at any position on its structure with substituents generally known in the art.

5 The insulin-like antisense oligonucleotide may comprise at least one modified base moiety for example, 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine,
10 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine,
15 pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. In another embodiment, the oligonucleotide comprises at least one modified sugar moiety, for example, arabinose, 2-fluoroarabinose, xylulose, and hexose.

20 In yet another embodiment, the oligonucleotide comprises at least one modified phosphate backbone selected from the group consisting of a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

 In yet another embodiment, the oligonucleotide is an -anomeric oligonucleotide.
25 An -anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual -units, the strands run parallel to each other (Gautier et al., 1987, Nucl. Acids Res. 15:6625-6641). The oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization-triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, *etc.*

30 Oligonucleotides of the invention may be synthesized by standard methods known in the art, *e.g.*, by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, *etc.*). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein et al. (Stein et al., 1988, Nucl.

Acids Res. 16:3209), methylphosphonate oligonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin et al., 1988, Proc. Natl. Acad. Sci. U.S.A. 85:7448-7451), *etc.*

In a specific embodiment, an insulin-like antisense oligonucleotide comprises catalytic RNA, or a ribozyme (*see e.g.*, PCT Publication WO 90/11364, published October 4, 1990; Sarver et al., 1990, Science 247:1222-1225). In another embodiment, the oligonucleotide is a 2'-O-methylribonucleotide (Inoue et al., 1987, Nucl. Acids Res. 15:6131-6148), or a chimeric RNA-DNA analogue (Inoue et al., 1987, FEBS Lett. 215:327-330).

In an alternative embodiment, the insulin-like antisense nucleic acid of the invention is produced intracellularly by transcription from an exogenous sequence. For example, a vector can be introduced *in vivo* such that it is taken up by a cell, within which cell the vector or a portion thereof is transcribed, producing an antisense nucleic acid (RNA) of the invention. Such a vector would contain a sequence encoding the insulin-like antisense nucleic acid. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art, used for replication and expression in mammalian cells. Expression of the sequence encoding the insulin-like antisense RNA can be by any promoter known in the art. Such promoters can be inducible or constitutive. Examples include the SV40 early promoter region (Benoist and Chambon, 1981, Nature 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto et al., 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner et al., 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster et al., 1982, Nature 296:39-42), *etc.*

The antisense nucleic acids of the invention comprise a sequence complementary to at least a sequence-specific portion of an RNA transcript of an insulin-like gene. However, absolute complementarity, although preferred, is not required. A sequence "complementary to at least a portion of an RNA," as referred to herein, means a sequence having sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded insulin-like antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to

hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an insulin-like RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine, e.g., the melting point of the hybridized complex.

Generating Gain-Of-Function Phenotypes By Ectopic Expression Of Insulin-Like Genes

The current invention provides methods for generating gain-of-function phenotypes by ectopic expression of insulin-like genes. Ectopic expression, including mis-expression or overexpression, of wild type or altered *Drosophila* insulin-like genes in transgenic animals is another useful method for the analysis of gene function (Brand, et al., 1994, Methods in Cell Biology 44:635-654, Ectopic expression in *Drosophila*; Hay, et al., 1997, Proc. Natl. Acad. Sci. U.S.A. 94(10):5195-200). Such transgenic *Drosophila* may be created that contain gene fusions of the coding regions of insulin-like genes (from either genomic DNA or cDNA) operably joined to a specific promoter and transcriptional enhancer whose regulation has preferably been well characterized, preferably heterologous promoters/enhancers that do not normally drive the expression of the insulin-like genes. Examples of promoters/enhancers that can be used to drive such misexpression of insulin-like genes include the heat shock promoters/enhancers from the *hsp70* and *hsp83* genes, useful for temperature induced expression; tissue specific promoters/enhancers such as the *sevenless* promoter/enhancer (Bowtell, et al., 1988, Genes Dev. 2(6):620-34), the *eyeless* promoter/enhancer (Bowtell, et al., 1991, Proc. Natl. Acad. Sci. U.S.A. 88(15):6853-7), and *glass*-responsive promoters/enhancers (Quiring, et al., 1994, Science 265:785-9) useful for expression in the eye; enhancers/promoters derived from the *dpp* or *retigal* genes useful for expression in the wing (Staehling-Hampton, et al., 1994, Cell Growth Differ. 5(6):585-93; Kim, et al., 1996, Nature 382:133-8) and binary control systems employing exogenous DNA regulatory elements and exogenous transcriptional activator proteins, useful for testing the misexpression of genes in a wide variety of developmental stage-specific and tissue-specific patterns. Two examples of binary exogenous regulatory systems include the UAS/GAL4 system from yeast (Hay, et al., 1997, Proc. Natl. Acad. Sci. U.S.A. 94(10):5195-200; Ellis, et al., 1993, Development

119(3):855-65) and the “Tet system” derived from *E. coli*, which are described below. It is readily apparent to those skilled in the art that additional binary systems can be used which are based on other sets of exogenous transcriptional activators and cognate DNA regulatory elements in a manner similar to that for the UAS/GAL4 system and the Tet system.

In a specific embodiment, the UAS/GAL4 system is used. This system is a well-established and powerful method of mis-expression in *Drosophila* which employs the UAS_G upstream regulatory sequence for control of promoters by the yeast GAL4 transcriptional activator protein (Brand and Perrimon, 1993, Development 118(2):401-15).

In this approach, transgenic *Drosophila*, termed “target” lines, are generated where the gene-of-interest (e.g. an insulin-like gene) to be mis-expressed is operably fused to an appropriate promoter controlled by UAS_G. Other transgenic *Drosophila* strains, termed “driver” lines, are generated where the GAL4 coding region is operably fused to promoters/enhancers that direct the expression of the GAL4 activator protein in specific tissues, such as the eye, wing, nervous system, gut, or musculature. The gene-of-interest is not expressed in the so-called target lines for lack of a transcriptional activator to “drive” transcription from the promoter joined to the gene-of-interest. However, when the UAS-target line is crossed with a GAL4 driver line, mis-expression of the gene-of-interest is induced in resulting progeny in a specific pattern that is characteristic for that GAL4 line. The technical simplicity of this approach makes it possible to sample the effects of directed mis-expression of the gene-of-interest in a wide variety of tissues by generating one transgenic target line with the gene-of-interest, and crossing that target line with a panel of pre-existing driver lines. A very large number of specific GAL4 driver lines have been generated previously and are available for use with this system.

In a second embodiment, a related method of directed mis-expression in *Drosophila* is used, that makes use of a tetracycline-regulated gene expression from *E. coli*, referred to as the “Tet system”. In this case, transgenic *Drosophila* driver lines are generated where the coding region for a tetracycline-controlled transcriptional activator (tTA) is operably fused to promoters/enhancers that direct the expression of tTA in a tissue-specific and/or developmental stage-specific manner. Also, transgenic *Drosophila* target lines are generated where the coding region for the gene-of-interest to be mis-expressed (e.g. an insulin-like gene) is operably fused to a promoter that possesses a tTA-responsive regulatory element. Here again, mis-expression of the gene-of-interest can

be induced in progeny from a cross of the target line with any driver line of interest; moreover, the use of the Tet system as a binary control mechanism allows for an additional level of tight control in the resulting progeny of this cross. When *Drosophila* food is supplemented with a sufficient amount of tetracycline, it completely blocks expression of the gene-of-interest in the resulting progeny. Expression of the gene-of-interest can be induced at will simply by removal of tetracycline from the food. Also, the level of expression of the gene-of-interest can be adjusted by varying the level of tetracycline in the food. Thus, the use of the Tet system as a binary control mechanism for mis-expression has the advantage of providing a means to control the amplitude and timing of mis-expression of the gene-of-interest, in addition to spatial control. Consequently, if a gene-of-interest (e.g. an insulin-like gene) has lethal or deleterious effects when mis-expressed at an early stage in development, such as the embryonic or larval stages, the function of the gene-of-interest in the adult can still be assessed using the Tet system, by adding tetracycline to the food during early stages of development and removing tetracycline later so as to induce mis-expression only at the adult stage.

Analysis Of Mutant Phenotypes

After isolation of fruit flies carrying mutated or mis-expressed insulin-like genes, or inhibitory RNAs, animals are carefully examined for phenotypes-of-interest. For the situations involving deletions, insertions, point mutations, or mis-expression of insulin-like genes, fruit flies are generated that are homozygous and heterozygous for the altered insulin-like genes.

Examples of specific phenotypes that may be investigated include : altered body shape, altered body size, lethality, sterility, reduced brood size, increased brood size, altered life span, defective locomotion, altered body plan, altered cell size, increased cell division, decreased cell division, altered feeding, slowed development, increased development, altered metabolism, (such as altered glycogen synthesis, storage, or degradation; altered lipid synthesis, storage or degradation; altered levels of carbohydrate in the hemolymph; and altered levels of lipid in the hemolymph), and altered morphogenesis of specific organs and tissues such as gonad, nervous system, fat body, hemocytes, peripheral sensory organs, bristles, imaginal discs, eye, wing, leg, antennae, gut, or musculature. For example, it is of particular interest to identify the ligand or ligands responsible for activating InR (or DIR), a *Drosophila* homologue of the insulin

receptor. A likely phenotype of a loss-of-function mutation in the ligand for the InR receptor might resemble one or more of the identified loss of function phenotypes for the receptor itself, including reduced body size and weight, reduced female fertility, increased developmental time, and/or defective embryonic neurogenesis.

5 Methods for creation and analysis of transgenic *Drosophila* strains having modified expression of genes are well known to those skilled in the art (Brand, et al., 1994, *Methods in Cell Biology* 44:635-654; Hay, et al., 1997, *Proc. Natl. Acad. Sci. USA* 94(10):5195-200). cDNAs or genomic regions encoding normal or mutant insulin-like genes can be operably fused to a desired promoter, as described above, and the
10 promoter-insulin-like gene fusion inserted into any appropriate *Drosophila* transformation vector for the generation of transgenic flies. Typically, such transformation vectors are based on a well-characterized transposable elements, for example the P element (Rubin and Spradling, 1982, *Science* 218:348-53), the hobo element (Blackman, et al., 1989, *Embo J.* 8(1):211-7), mariner element (Lidholm, et al., 1993, *Genetics* 134(3):859-68), the
15 hermes element (O'Brochta, et al., 1996, *Genetics* 142(3):907-14), Minos (Loukeris, et al., 1995, *Proc. Natl. Acad. Sci. USA* 92(21):9485-9), or the PiggyBac element (Handler, et al., 1998, *Proc. Natl. Acad. Sci. USA* 95(13):7520-5), where the terminal repeat sequences of the transposon that are required for transposition are incorporated into the transformation vector and arranged such that the terminal repeat sequences flank the
20 transgene of interest (in this case a promoter-insulin-like gene fusion) as well as a marker gene used to identify transgenic animals. Most often, marker genes are used that affect the eye color of *Drosophila*, such as derivatives of the *Drosophila white* or *rosy* genes; however, in principle, any gene can be used as a marker that causes a reliable and easily scored phenotypic change in transgenic animals, and examples of other marker genes used
25 for transformation include the *Adh*⁺ gene used as a selectable marker for the transformation of *Adh*⁻ strains, *Ddc*⁺ gene used to transform *Ddc*^{ts2} mutant strains, the *lacZ* gene of *E. coli*, and the *neomycin*^R gene from the *E. coli* transposon Tn5. Plasmid constructs for introduction of the desired transgene are coinjected into *Drosophila* embryos having an appropriate genetic background, along with a helper plasmid that
30 expresses the specific transposase need to mobilized the transgene into the genomic DNA. Animals arising from the injected embryos (G0 adults) are selected, or screened manually, for transgenic mosaic animals based on expression of the marker gene phenotype and are subsequently crossed to generate fully transgenic animals (G1 and subsequent generations)

that will stably carry one or more copies of the transgene of interest. Such stable transgenic animals are inspected for mutant phenotypes, such as abnormal development, morphology, metabolism, growth, longevity, reproduction, viability, or behavior, in order to determine a function for the insulin-like gene created by ectopic expression or overexpression of the insulin-like gene, or by expression of mutant insulin-like genes.

Generation of an overexpression/mis-expression phenotype is likely to result from either activation or inhibition of a receptor-linked signaling pathway. If such an overexpression/mis-expression phenotype is defined for an insulin-like gene, clonal analysis can then be used to determine whether this phenotype is restricted to cells expressing the insulin-like gene (i.e. whether the phenotype is cell autonomous or cell non-autonomous). Methods of mitotic recombination of chromosomes in heterozygous flies can be used to generate mitotic clones of genetically homozygous cells that are well known to those skilled in the art, which include the use of X-rays or preferably FLP/FRT mediated recombination (Xu and Harrison, 1994, *Methods in Cell Biology* 44:655-681; Greenspan, 1979, In *Fly Pushing: The Theory and Practice of Drosophila Genetics*. Plainview, NY, Cold Spring Harbor Laboratory Press: pp. 103-124). These mitotic recombination techniques result in patches of cells, mitotic clones, that contain 2 or no copies of the gene-of-interest. Production of the overexpression/mis-expression phenotype within cells in a clone having no copies of the gene-of-interest indicates that the effect is not cell autonomous, and is therefore likely to be the effect of a secreted molecule, as might be expected for insulin-like molecules.

Identification of Molecules that Interact With Insulin-Like Proteins

A variety of methods can be used to identify or screen for molecules, such as proteins or other molecules, that interact with insulin-like protein, or derivatives or fragments thereof. The assays may employ purified insulin-like protein, or cell lines or model organisms such as *Drosophila* and *C. elegans*, that have been genetically engineered to express insulin-like protein. Suitable screening methodologies are well known in the art to test for proteins and other molecules that interact with insulin-like gene and protein (see e.g., PCT International Publication No. WO 96/34099). The newly identified interacting molecules may provide new targets for pharmaceutical or pesticidal agents. Any of a variety of exogenous molecules, both naturally occurring and/or synthetic (e.g., libraries of small molecules or peptides, or phage display

libraries), may be screened for binding capacity. In a typical binding experiment, the insulin-like protein or fragment is mixed with candidate molecules under conditions conducive to binding, sufficient time is allowed for any binding to occur, and assays are performed to test for bound complexes. Assays to find interacting proteins can be performed by any method known in the art, for example, immunoprecipitation with an antibody that binds to the protein in a complex followed by analysis by size fractionation of the immunoprecipitated proteins (*e.g.* by denaturing or nondenaturing polyacrylamide gel electrophoresis), Western analysis, non-denaturing gel electrophoresis, *etc.*

Two-hybrid assay systems

A preferred method for identifying interacting proteins is a two-hybrid assay system or variation thereof (Fields and Song, *Nature* (1989) 340:245-246; U.S. Pat. No. 5,283,173; for review see Brent and Finley, *Annu. Rev. Genet.* (1997) 31:663-704).

The most commonly used two-hybrid screen system is performed using yeast. All systems share three elements: 1) a gene that directs the synthesis of a "bait" protein fused to a DNA binding domain; 2) one or more "reporter" genes having an upstream binding site for the bait, and 3) a gene that directs the synthesis of a "prey" protein fused to an activation domain that activates transcription of the reporter gene. For the screening of proteins that interact with insulin-like protein, the "bait" is preferably a insulin-like protein, expressed as a fusion protein to a DNA binding domain; and the "prey" protein is a protein to be tested for ability to interact with the bait, and is expressed as a fusion protein to a transcription activation domain. The prey proteins can be obtained from recombinant biological libraries expressing random peptides.

The bait fusion protein can be constructed using any suitable DNA binding domain, such as the *E. coli* LexA repressor protein, or the yeast GAL4 protein (Bartel *et al.*, *BioTechniques* (1993) 14:920-924, Chasman *et al.*, *Mol. Cell. Biol.* (1989) 9:4746-4749; Ma *et al.*, *Cell* (1987) 48:847-853; Ptashne *et al.*, *Nature* (1990) 346:329-331).

The prey fusion protein can be constructed using any suitable activation domain such as GAL4, VP-16, *etc.* The preys may contain useful moieties such as nuclear localization signals (Ylikomi *et al.*, *EMBO J.* (1992) 11:3681-3694; Dingwall and Laskey, *Trends Biochem. Sci.* (1991) 16:479-481) or epitope tags

(Allen *et al.*, Trends Biochem. Sci. Trends Biochem. Sci. (1995) 20:511-516) to facilitate isolation of the encoded proteins.

Any reporter gene can be used that has a detectable phenotype such as reporter genes that allow cells expressing them to be selected by growth on appropriate medium (e.g. HIS3, LEU2 described by Chien *et al.*, PNAS (1991) 88:9572-9582; and Gyuris *et al.*, Cell (1993) 75:791-803). Other reporter genes, such as LacZ and GFP, allow cells expressing them to be visually screened (Chien *et al.*, *supra*).

Although the preferred host for two-hybrid screening is the yeast, the host cell in which the interaction assay and transcription of the reporter gene occurs can be any cell, such as mammalian (e.g. monkey, mouse, rat, human, bovine), chicken, bacterial, or insect cells. Various vectors and host strains for expression of the two fusion protein populations in yeast can be used (U.S. Pat. No. 5,468,614; Bartel *et al.*, Cellular Interactions in Development (1993) Hartley, ed., Practical Approach Series xviii, IRL Press at Oxford University Press, New York, NY, pp. 153-179; and Fields and Sternglanz, Trends In Genetics (1994) 10:286-292). As an example of a mammalian system, interaction of activation tagged VP16 derivatives with a GAL4-derived bait drives expression of reporters that direct the synthesis of hygromycin B phosphotransferase, chloramphenicol acetyltransferase, or CD4 cell surface antigen (Fearon *et al.*, PNAS (1992) 89:7958-7962). As another example, interaction of VP16-tagged derivatives with GAL4-derived baits drives the synthesis of SV40 T antigen, which in turn promotes the replication of the prey plasmid, which carries an SV40 origin (Vasavada *et al.*, PNAS (1991) 88:10686-10690).

Typically, the bait insulin-like gene and the prey library of chimeric genes are combined by mating the two yeast strains on solid or liquid media for a period of approximately 6-8 hours. The resulting diploids contain both kinds of chimeric genes, i.e., the DNA-binding domain fusion and the activation domain fusion.

Transcription of the reporter gene can be detected by a linked replication assay in the case of SV40 T antigen (described by Vasavada *et al.*, *supra*) or using immunoassay methods, preferably as described in Alam and Cook (Anal. Biochem. (1990) 188:245-254). The activation of other reporter genes like URA3, HIS3, LYS2, or LEU2 enables the cells to grow in the absence of uracil, histidine, lysine, or leucine, respectively, and hence serves as a selectable marker. Other types of reporters are

monitored by measuring a detectable signal. For example, GFP and lacZ have gene products that are fluorescent and chromogenic, respectively.

After interacting proteins have been identified, the DNA sequences encoding the proteins can be isolated. In one method, the activation domain sequences or DNA-binding domain sequences (depending on the prey hybrid used) are amplified, for example, by PCR using pairs of oligonucleotide primers specific for the coding region of the DNA binding domain or activation domain. Other known amplification methods can be used, such as ligase chain reaction, use of Q replicase, or various other methods described (see Kricka *et al.*, Molecular Probing, Blotting, and Sequencing (1995) Academic Press, New York, Chapter 1 and Table IX). If a shuttle (yeast to *E. coli*) vector is used to express the fusion proteins, the DNA sequences encoding the proteins can be isolated by transformation of *E. coli* using the yeast DNA and recovering the plasmids from *E. coli*. Alternatively, the yeast vector can be isolated, and the insert encoding the fusion protein subcloned into a bacterial expression vector, for growth of the plasmid in *E. coli*.

Immunoassays

Immunoassays can be used to identify proteins that interact with or bind to insulin-like protein. Various assays are available for testing the ability of a protein to bind to or compete with binding to a wild-type insulin-like protein or for binding to an anti-insulin-like protein antibody. Suitable assays include radioimmunoassays, ELISA (enzyme linked immunosorbent assay), immunoradiometric assays, gel diffusion precipitin reactions, immunodiffusion assays, *in situ* immunoassays (*e.g.*, using colloidal gold, enzyme or radioisotope labels), western blots, precipitation reactions, agglutination assays (*e.g.*, gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, immunoelectrophoresis assays, *etc.*

Biochemical Assays Using Insulin-Like Proteins

The present invention provides for biochemical assays using the insulin-like proteins. In one embodiment, *Drosophila* insulin-like proteins are useful for biochemical assays aimed at the identification and characterization of the ligand(s) for the known *Drosophila* insulin receptor encoded by the *InR* (DIR) gene (Nishida, et al., 1986,

Biochem. Biophys. Res. Commun. 141(2):474-81; Petruzzelli, et al., 1986, Proc. Natl. Acad. Sci. U.S.A. 83(13):4710-4; Fernandez-Almonacid and Rosen, 1987, Mol. Cell Biol. 7(8):2718-27), or the identification of ligands for new insulin-like receptor proteins that are discovered. The cDNAs encoding the insulin-like proteins can be individually
5 subcloned into any of a large variety of eukaryotic expression vectors permitting expression in insect and mammalian cells, described above. The resulting genetically engineered cell lines expressing insulin-like proteins can be assayed for production, processing, and secretion of the mature insulin-like proteins, which lack the secretory signal peptide and connecting C peptide regions, for example with antibodies to
10 *Drosophila* insulin-like proteins and Western blotting assays or ELISA assays. For assays of specific receptor binding and functional activation of receptor proteins, one can employ either crude culture medium or extracts containing secreted protein from genetically engineered cells (devoid of other insulin proteins), or partially purified culture medium or extracts, or preferably highly purified *Drosophila* insulin-like protein fractionated, for
15 example, by chromatographic methods. Alternatively, mature *Drosophila* insulin-like protein can be synthesized using chemical methods (Nagata, et al., 1992, peptides 13(4):653-62).

Specific protein binding of *Drosophila* insulin-like proteins to the *Drosophila* InR receptor can be assayed as follows, for example, following the procedures of Yamaguchi
20 et al. (Yamaguchi et al., 1995, Biochemistry 34:4962-4968). Chinese hamster ovary cells, COS cells, or any other suitable cell line, can be transiently transfected or stably transformed with expression constructs that direct the production of the *Drosophila* insulin receptor InR. Direct binding of a *Drosophila* insulin-like protein to such InR-expressing cells can be measured using a "labeled" purified *Drosophila* insulin-like protein
25 derivative, where the label is typically a chemical or protein moiety covalently attached to the insulin-like polypeptide which permits the experimental monitoring and quantitation of the labeled *Drosophila* insulin-like protein in a complex mixture.

Specifically, the label attached to the insulin-like protein can be a radioactive substituent such as an ¹²⁵I-moiety or ³²P-phosphate moiety, a fluorescent chemical
30 moiety, or labels which allow for indirect methods of detection such as a biotin-moiety for binding by avidin or streptavidin, an epitope-tag such as a Myc- or FLAG-tag, or a protein fusion domain which allows for direct or indirect enzymatic detection such as an alkaline phosphatase-fusion or Fc-fusion domain. Such labeled *Drosophila* insulin-like

proteins can be used to test for direct and specific binding to InR-expressing cells by incubating the labeled *Drosophila* insulin-like protein with the InR-expressing cells in serum-free medium, washing the cells with ice-cold phosphate buffered saline to remove unbound insulin-like protein, lysing the cells in buffer with an appropriate detergent, and measuring label in the lysates to determine the amount of bound insulin-like protein. Alternatively, in place of whole cells, membrane fractions obtained from InR-expressing cells may also be used. Also, instead of a direct binding assay, a competition binding assay may be used. For example, crude extracts or purified *Drosophila* insulin-like protein can be used as a competitor for binding of labeled purified bovine or porcine insulin to InR-expressing cells, by adding increasing concentrations of *Drosophila* insulin-like protein to the mixture. The specificity and affinity of binding of *Drosophila* insulin-like proteins can be judged by comparison with other insulin superfamily proteins tested in the same assay, for example vertebrate insulin, vertebrate IGF-I, vertebrate IGF-II, vertebrate relaxin, or silkmom bombyxin.

Identification Of Additional Receptors Or Insulin-Like Binding Proteins

The invention described herein provides for methods in which *Drosophila* insulin-like proteins are used for the identification of novel insulin receptor proteins, other than *Drosophila* InR, using biochemical methods well known to those skilled in the art for detecting specific protein-protein interactions (Current Protocols in Protein Science, 1998, Coligan et al., eds., John Wiley & Sons, Inc., Somerset, New Jersey). Given the sequence diversity of the *Drosophila* insulin-like proteins detailed herein, the identification to date of only a single insulin receptor gene in *Drosophila*, *InR*, points to the possibility that some *Drosophila* insulin-like proteins may bind to other receptors.

In particular, it is possible that some *Drosophila* insulin-like proteins interact with receptor types that have not yet been discovered in vertebrates, for example the relaxin receptor, or receptor types that are specific to invertebrates. The identification of either novel receptor types or invertebrate-specific receptor types is of great interest with respect to human therapeutic applications, or pesticide applications, respectively.

Assuming some *Drosophila* insulin-like proteins do not exhibit specific protein binding to the known InR protein in the binding assays described above, then the novel cognate receptors for these insulin-like proteins can be investigated and identified as follows. Labeled *Drosophila* insulin-like proteins can be used for binding assays *in situ* to

identify tissues and cells possessing cognate receptors, for example as described elsewhere (Gorczyca et al., 1993, J. Neurosci. 13:3692-3704). Also, labeled *Drosophila* insulin-like proteins can be used to identify specific binding proteins including receptor proteins by affinity chromatography of *Drosophila* protein extracts using resins, beads, or chips with bound *Drosophila* insulin-like protein (Formosa, et al., 1991, Methods Enzymol 208:24-45; Formosa, et al., 1983, Proc. Natl. Acad. Sci. USA 80(9):2442-6). Further, specific insulin-binding proteins can be identified by cross-linking of radioactively-labeled or epitope-tagged insulin-like protein to specific binding proteins in lysates, followed by electrophoresis to identify and isolate the cross-linked protein species (Ransone, 1995, Methods Enzymol 254:491-7). Still further, molecular cloning methods can be used to identify novel receptors and binding proteins for *Drosophila* insulin-like proteins including expression cloning of specific receptors using *Drosophila* cDNA expression libraries transfected into mammalian cells, expression cloning of specific binding proteins using *Drosophila* cDNA libraries expressed in *E. coli* (Cheng and Flanagan, 1994, Cell 79(1):157-68), and yeast two-hybrid methods (as described above) using a *Drosophila* insulin-like protein fusion as a "bait" for screening activation-domain fusion libraries derived from *Drosophila* cDNA (Young and Davis, 1983, Science 222(4625):778-82; Young and Davis, 1983, Proc. Natl. Acad. Sci. USA 80(5):1194-8; Sikela and Hahn, 1987, Proc. Natl. Acad. Sci. USA 84(9):3038-42; Takemoto, et al., 1997, DNA Cell Biol 16(6):797-9).

ASSAYS OF INSULIN-LIKE PROTEINS

The functional activity of insulin-like proteins, derivatives and analogs can be assayed by various methods known to one skilled in the art.

For example, in one embodiment, where one is assaying for the ability to bind to or compete with a wild-type insulin-like protein for binding to an anti-insulin-like protein antibody, various immunoassays known in the art can be used, including competitive and non-competitive assay systems using techniques such as radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitin reactions, immunodiffusion assays, *in situ* immunoassays (e.g., using colloidal gold, enzyme or radioisotope labels), western blots, precipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, and

immuno-electrophoresis assays, *etc.* In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labeled. Many means are known in the art for detecting binding in an immunoassay and are within the scope of the present invention. In another embodiment, where an insulin-like-binding protein is identified, the binding can be assayed, *e.g.*, by means well-known in the art. In another embodiment, physiological correlates of insulin-like protein binding to its substrates and/or receptors (*e.g.*, signal transduction) can be assayed.

In another embodiment, in insect (*e.g.*, Sf9 cells), fly (*e.g.*, *D. melanogaster*), or other model systems, genetic studies can be done to study the phenotypic effect of an insulin-like gene mutant that is a derivative or analog of a wild-type insulin-like gene. Other such methods will be readily apparent to the skilled artisan and are within the scope of the invention.

Other Functional Assays

For functional assays of *Drosophila* insulin-like protein, beyond receptor binding, the following activities can be investigated using InR-expressing cells after exposing said cells to crude or purified fractions of *Drosophila* insulin-like protein and comparing these results with those obtained with other insulin superfamily proteins described above (Yamaguchi et al., 1995, Biochemistry 34:4962-4968). Assayable functional activities include stimulation of cell proliferation; stimulation of overall tyrosine kinase activity by immunoblotting of cell extracts with an anti-phosphotyrosine antibody; stimulation of phosphorylation of specific substrate proteins such as InR or IRS-1 using ³²P- labeling and immunoprecipitation with antibodies that specifically recognize the substrate protein; and stimulation of other enzymatic activities linked to the insulin signaling pathway including assays of MAP kinase, Mek kinase, Akt kinase, and PI3-kinase activities.

Identifying Signaling Pathways And Phenotypes

This invention provides animal models which may be used in the identification and characterization of *D. melanogaster* insulin-like protein signaling pathways, and/or phenotypes associated with the mutation or abnormal expression of a *D. melanogaster* insulin-like protein. Methods of producing such animal models using novel genes and

proteins are well known in the art (*see e.g.*, PCT International Publication No. WO 96/34099, published October 31, 1996, which is incorporated by reference herein in its entirety). Such models include but are not limited to the following embodiments.

Additional specific examples of animal models and their use are described below.

5 First, animals are provided in which a normal *D. melanogaster* insulin-like gene has been recombinantly introduced into the genome of the animal as an additional gene, under the regulation of either an exogenous or an endogenous promoter element, and as either a minigene or a large genomic fragment. Animals are also provided in which a normal gene has been recombinantly substituted for one or both copies of the animal's
10 homologous gene by homologous recombination or gene targeting.

Second, animals are provided in which a mutant *D. melanogaster* insulin-like gene has been recombinantly introduced into the genome of the animal as an additional gene, under the regulation of either an exogenous or an endogenous promoter element, and as either a minigene or a large genomic fragment. Animals are also provided in which a
15 mutant gene has been recombinantly substituted for one or both copies of the animal's homologous gene by homologous recombination or gene targeting.

Third, animals are provided in which a mutant version of one of that animal's own genes (bearing, for example, a specific mutation corresponding to, or similar to, a pathogenic mutation of an insulin-like gene from another species) has been recombinantly
20 introduced into the genome of the animal as an additional gene, under the regulation of either an exogenous or an endogenous promoter element, and as either a minigene or a large genomic fragment.

Finally, equivalents of transgenic animals, including animals with mutated or inactivated genes, may be produced using chemical or x-ray mutagenesis. Using the
25 isolated nucleic acids disclosed or otherwise enabled herein, one of ordinary skill may more rapidly screen the resulting offspring by, for example, direct sequencing, restriction fragment length polymorphism (RFLP) analysis, PCR, or hybridization analysis to detect mutants, or Southern blotting to demonstrate loss of one allele.

Such animal models may be used to identify a *D. melanogaster* insulin-like protein
30 signaling pathway by various methods. In one embodiment, this invention provides a method of identifying a *D. melanogaster* insulin-like protein signaling pathway comprising: (a) disrupting a *D. melanogaster* insulin-like gene; and (b) identifying the effect of the gene disrupted in step (a) in an assay selected from the group consisting of a

developmental assay, an energy metabolism assay, a growth rate assay and a reproductive capacity assay, lethality, sterility, reduced brood size, increased brood size, altered life span, defective locomotion, altered body shape, altered body plan, altered body size, altered bristles, altered body weight, altered cell size, increased cell division, decreased cell division, altered feeding, slowed development, increased development, decreased metabolism (including alterations in glycogen synthesis, storage, and/or degradation, alterations in lipid synthesis, storage and/or degradation, alterations in levels of carbohydrate in hemolymph, alterations in levels of lipid in hemolymph), alterations in morphogenesis (including organs or tissues of the gonad, nervous system, fat body, hemocytes, peripheral sensory organs, imaginal discs, eye, wing, leg, antennae, bristle, gut or musculature). Such assays are well known to those skilled in the art. In one embodiment, results of the assay may be compared to known mutant phenotypes to determine the signaling pathway involved. In one embodiment, the gene is disrupted using chemical mutagenesis. In another embodiment, the gene is disrupted using transposon mutagenesis. In a further embodiment, the gene is disrupted by radiation mutagenesis.

Further, this invention provides a method of identifying a phenotype associated with mutation or abnormal expression of a *D. melanogaster* insulin-like protein comprising identifying the effect of a mutated or abnormally expressed *D. melanogaster* insulin-like gene in a *D. melanogaster* animal. In one embodiment, the effect is determined by any of the assays mentioned above in connection with identifying a *D. melanogaster* insulin-like protein signaling pathway. The gene may be mutated or abnormally expressed using any technique known in the art, such chemical mutagenesis, radiation mutagenesis, transposon mutagenesis, antisense and double-stranded RNA interference. Abnormal (i.e. ectopic) expression can be overexpression, underexpression (e.g., due to inactivation), expression at a developmental time different from wild-type animals, or expression in a cell type different from in wild-type animals.

Analysis Of Genetic Interactions And Multiple Mutants

Yet another approach that may be used to probe the biological function of the insulin-like genes identified herein is by using tests for genetic interactions with other genes that may participate in the same, related, interacting, or modifying genetic or biochemical pathways. In particular, since it is evident that there are multiple insulin-like genes in the *Drosophila* genome, this raises the possibility of functional redundancy of one or more genes. Consequently, it is of interest to investigate the phenotypes of fruit flies

containing mutations that eliminate the function of more than one insulin-like gene. Such strains carrying mutations in multiple genes can be generated by cross breeding animals carrying the individual mutations, followed by selection of recombinant progeny that carry the desired multiple mutations.

5 One specific question-of-interest is genetic analysis of interactions of insulin-like genes with other well-characterized *Drosophila* genes and pathways. Thus, double mutant fruit flies may be constructed that carry mutations in an insulin-like gene and another gene-of-interest.

It is of particular interest to test the interaction of the insulin-like genes with other
10 genes implicated in insulin signaling, especially those that exhibit homology to insulin signaling components in vertebrates. For example, fruit flies carrying mutations in insulin-like genes and either a loss-of-function mutation of *InR*, *chico*, *Pi3K92*, *Akt1*, *14-3-3z*, *csw*, *Lar*, *Pk61C*, *Glut3*, *Ide*, *shaggy*, *s6k*, *Ras85D*, *drk*, *Sos*, *rl*, or *Dsor1* (FlyBase 1998, "FlyBase - A *Drosophila* Database", Nucleic Acids Research 26:85-88;
15 <http://flybase.bio.indiana.edu>), would be of use in investigating the involvement of different insulin-like genes in the signaling pathway where these genes participate. Similarly, transgenic animals mis-expressing insulin-like genes which further carry mutations in the above-mentioned genes are of also of interest. Other genetic interactions may be tested based on the actual phenotypes observed for alterations of the insulin-like
20 genes alone.

Genetic Modifier Screens

The initial characterization of phenotypes created by mutations in single or multiple insulin-like genes is expected to lead to the identification of *Drosophila* strains
25 that exhibit mutant phenotypes suitable for large scale genetic modifier screens aimed at discovering other components of the same pathway. The procedures involved in typical genetic modifier screens to define other components of a genetic/biochemical pathway are well known to those skilled in the art and have been described elsewhere (Wolfner and Goldberg, 1994, Methods in Cell Biology 44:33-80; Karim et al., 1996, Genetics
30 143:315-329). Such genetic modifier screens are based on the identification of mutations in other genes that modify an initial mutant phenotype, by isolating either suppressor mutations that return the mutant phenotype toward normal, or enhancer mutations that make the initial mutant phenotype more severe.

Standard Genetic Modifier Screens

Genetic modifier screens differ depending upon the precise nature of the mutant allele being modified. If the mutant allele is genetically recessive, as is commonly the situation for a loss-of-function allele, then most typically males, or in some cases females, which carry one copy of the mutant allele are exposed to an effective mutagen, such as EMS, MMS, ENU, triethylamine, diepoxyalkanes, ICR-170, formaldehyde, X-rays, gamma rays, or ultraviolet radiation. The mutagenized animals are crossed to animals of the opposite sex that also carrying the mutant allele to be modified, and the resulting progeny are scored for rare events that result in a suppressed or enhanced version of the original mutant phenotype. In the case where the mutant allele being modified is genetically dominant, as is commonly the situation for ectopically expressed genes, wild type males are mutagenized and crossed to females carrying the mutant allele to be modified. Any new mutations identified as modifiers (i.e. suppressors or enhancers) are candidates for genes that participate in the same phenotype-generating pathway.

In a pilot-scale genetic modifier screen, 10,000 or fewer mutagenized progeny are inspected; in a moderate size screen, 10,000 to 50,000 mutagenized progeny are inspected; and in a large scale screen, over 50,000 mutagenized progeny are inspected. Progeny exhibiting either enhancement or suppression of the original phenotype are immediately crossed to adults containing balancer chromosomes and used as founders of a stable genetic line. In addition, progeny of the founder adult are retested under the original screening conditions to ensure stability and reproducibility of the phenotype. Additional secondary screens may be employed, as appropriate, to confirm the suitability of each new modifier mutant line for further analysis. For example, newly identified modifier mutations can be tested directly for interaction with other genes of interest known to be involved or implicated in insulin signaling pathways (*InR*, *chico*, *Pi3K92*, *Atk1*, *14-3-3z*, *csw*, *Lar*, *Pk61C*, *Glut3*, *Ide*, *shaggy*, *s6k*, *Ras85D*, *drk*, *Sos*, *rl*, *Dsor1*, mutations in other insulin-like genes, or other modifier genes obtained from different genetic screens of the insulin signaling pathway), using methods described above. Also, the new modifier mutations can be tested for interactions with genes in other pathways thought to be unrelated or distantly related to insulin signaling, such as genes in the *Notch* signaling pathway. New modifier mutations that exhibit specific genetic interactions with other genes implicated in insulin signaling, but not interactions with genes in unrelated

pathways, are of particular interest. Additionally, strains can be generated that carry the new modifier mutations of interest in the absence of the original insulin-like gene mutation (i.e. a strain wild type for the mutant allele being suppressed or enhanced) to determine whether the new modifier mutation exhibits an intrinsic phenotype, independent of the mutation in the insulin-like gene, which might provide further clues as to the normal function of the new modifier gene.

Each newly-identified modifier mutation can be crossed to other modifier mutations identified in the same screen to place them into complementation groups, which typically correspond to individual genes (Greenspan, 1997, In *Fly Pushing: The Theory and Practice of Drosophila Genetics*, Plainview, NY, Cold Spring Harbor Laboratory Press: pp. 23-46). Two modifier mutations are said to fall within the same complementation group if animals carrying both mutations in *trans* exhibit essentially the same phenotype as animals that are homozygous for each mutation individually.

Gain-Of-Function Modifier Screens

Although the genetic modifier screens described above are quite powerful and sensitive, some genes that participate in an insulin-like pathway may be missed in this approach, particularly if there is functional redundancy of those genes. This is because the vast majority of the mutations generated in the standard mutagenesis methods described above will be loss-of-function mutations, whereas gain-of-function mutations that could reveal genes with functional redundancy will be relatively rare. Another method of genetic screening in *Drosophila* has been developed that focuses specifically on systematic gain-of-function genetic screens (Rorth, et al., 1998, Development 125:1049-1057). This method is based on a modular mis-expression system utilizing components of the GAL4/UAS system (which were defined above). In this case a modified P element, termed an EP element, is genetically engineered to contain a GAL4-responsive UAS element and promoter, and this engineered transposon is used to randomly tag genes by insertional mutagenesis (similar to the method of P mutagenesis described above). Thousands of transgenic *Drosophila* strains, termed EP lines, can thus be generated each containing a specific UAS-tagged gene. This approach takes advantage of a well-recognized insertional preference of P elements, where it has been found that P elements have a strong tendency to insert at the 5'-ends of genes. Consequently, many of the genes that have been tagged by insertion of EP elements become operably fused to a

GAL4-regulated promoter, and increased expression or mis-expression of the randomly tagged gene can be induced by crossing in a GAL4 driver gene (similar that described above).

Thus, systematic gain-of-function genetic screens for modifiers of phenotypes induced by mutation or mis-expression of an insulin-like gene can be performed as follows. A large battery of thousands of *Drosophila* EP lines can be crossed into a genetic background containing a mutant or mis-expressed insulin-like gene, and further containing an appropriate GAL4 driver transgene. The progeny of this cross can be inspected for enhancement or suppression of the original phenotype induced by mutation/mis-expression of the insulin-like gene. Progeny that exhibit an enhanced or suppressed phenotype can be crossed further to verify the reproducibility and specificity of this genetic interaction with the insulin-like gene. EP insertions that demonstrate a specific genetic interaction with a mutant or mis-expressed insulin-like gene, have therefore physically tagged a new gene that genetically interacts with the insulin-like. The new modifier gene can be identified and sequenced using PCR or hybridization screening methods that allow the isolation of the genomic DNA adjacent to the position of the EP element insertion.

Assays For Changes In Gene Expression

This invention provides assays for detecting changes in the expression of the *D. melanogaster* insulin-like genes and proteins. Assays for changes in gene expression are well known in the art (*see e.g.*, PCT Publication No. WO 96/34099, published October 31, 1996, which is incorporated by reference herein in its entirety). Such assays may be performed *in vitro* using transformed cell lines, immortalized cell lines, or recombinant cell lines, or *in vivo* using animal models.

In particular, the assays may detect the presence of increased or decreased expression of a *D. melanogaster* insulin-like gene or protein on the basis of increased or decreased mRNA expression (using, *e.g.*, nucleic acid probes), increased or decreased levels of related protein products (using, *e.g.*, the antibodies disclosed herein), or increased or decreased levels of expression of a marker gene (*e.g.*, -galactosidase or luciferase) operably linked to a 5' regulatory region in a recombinant construct.

In yet another series of embodiments, various expression analysis techniques may be used to identify genes which are differentially expressed between two conditions, such as a cell line or animal expressing a normal *D. melanogaster* insulin-like gene compared to

another cell line or animal expressing a mutant *D. melanogaster* insulin-like gene. Such techniques comprise any expression analysis technique known to one skilled in the art, including differential display, serial analysis of gene expression (SAGE), nucleic acid array technology, subtractive hybridization, proteome analysis and mass-spectrometry of two-dimensional protein gels. In a specific embodiment, nucleic acid array technology (i.e., gene chips) may be used to determine a global (i.e., genome-wide) gene expression pattern in a normal *D. melanogaster* animal for comparison with an animal having a mutation in one or more *D. melanogaster* insulin-like genes.

To elaborate further, the various methods of gene expression profiling mentioned above can be used to identify other genes (or proteins) that may have a functional relation to (e.g., may participate in a signaling pathway with) a *D. melanogaster* insulin-like gene. Gene identification of such other genes is made by detecting changes in their expression levels following mutation, i.e., insertion, deletion or substitution in, or overexpression, underexpression, mis-expression or knock-out, of a *D. melanogaster* insulin-like gene, as described herein. Expression profiling methods thus provide a powerful approach for analyzing the effects of mutation in a *D. melanogaster* insulin-like gene.

Insulin-Like Gene Regulatory Elements

This invention provides methods for using insulin-like gene regulatory DNA elements to identify tissues, cells, genes and factors that specifically control insulin-like protein production. In one embodiment, regulatory DNA elements, such as enhancers/promoters, from *Drosophila* insulin-like genes are useful for identifying and manipulating specific cells and tissues that synthesize an insulin-like protein. Such hormone secreting cells and tissues are of considerable interest since they are likely to have an important regulatory function within the animal in sensing and controlling growth, development, reproduction, and/or metabolism. Analyzing components that are specific to insulin-like protein secreting cells is likely to lead to an understanding of how to manipulate these regulatory processes, either for therapeutic applications or pesticide applications, as well as an understanding of how to diagnose dysfunction in these processes. For example, it is of specific interest to investigate whether there are neuroendocrine tissues in *Drosophila* that might have a function related to that of the mammalian pancreas in sensing and controlling metabolic activity through the production of an insulin-like protein. Regulatory DNA elements derived from insulin-like genes

provide a means to mark and manipulate such cells, and further, identify regulatory genes and proteins, as described below.

Gene Fusions With Insulin-Like Gene Regulatory DNA Elements

In a specific embodiment, gene fusions with the insulin-like regulatory elements can be made. For compact genes that have relatively few and small intervening sequences, such as the insulin-like genes described here, it is typically the case that the regulatory elements that control spatial and temporal expression patterns are found in the DNA immediately upstream of the coding region, extending to the nearest neighboring gene.

Thus, putative regulatory DNA regions can be defined for the dIns2, dIns3, and dIns4 genes based on the sequence information provided in FIG.4. As shown in FIG. 4, the putative promoters ("PUT PROMOTER" or "PUT PROM") of the insulin-like genes are indicated with heavy lines below the respective sequences. Regulatory regions can be used to construct gene fusions where the regulatory DNAs are operably fused to a coding region for a reporter protein whose expression is easily detected, and these constructs are introduced as transgenes into *Drosophila*. An entire regulatory DNA region can be used, or the regulatory region can be divided into smaller segments to identify subelements that might be specific for controlling expression a given cell type or stage of development.

Examples of reporter proteins that can be used for construction of these gene fusions include *E. coli* beta-galactosidase or the fluorescent GFP protein whose products can be detected readily in situ and which are useful for histological studies (O'Kane and Gehring, 1987, Proc. Natl. Acad. Sci. U.S.A. 84(24):9123-7; Chalfie, et al., 1994, Science 263:802-805) and sorting of specific cells that express insulin-like proteins (Cumberledge and Krasnow, 1994, Methods in Cell Biology 44:143-159); the cre or FLP recombinase proteins that can be used to control the presence and expression of other genes in the same cells through site-specific recombination (Golic and Lindquist, 1989, Cell 59(3):499-509; White, et al., 1996, Science 271:805-7); toxic proteins such as the reaper and hid cell death proteins which are useful to specifically ablate cells that normally express insulin-like proteins in order to assess the physiological function of this tissue (Kingston, 1998, In *Current Protocols in Molecular Biology*. Ausubel et al., John Wiley & Sons, Inc. sections 12.0.3-12.10) or any other protein where it is desired to examine the function this particular protein specifically in cells that synthesize and secrete insulin-like proteins (as described in the mis-expression analysis above).

Alternatively, a binary reporter system can be used, similar to that described above, where the insulin-like regulatory element is operably fused to the coding region of an exogenous transcriptional activator protein, such as the GAL4 or tTA activators described above, to create an insulin-like regulatory element "driver gene". For the other half of the binary system the exogenous activator controls a separate "target gene" containing a coding region of a reporter protein operably fused to a cognate regulatory element for the exogenous activator protein, such as UAS_G or a tTA-response element, respectively. An advantage of a binary system is that a single driver gene construct can be used to activate transcription from preconstructed target genes encoding different reporter proteins, each with its own uses as delineated above.

The insulin-like regulatory element-reporter gene fusions described in the preceding paragraph are also useful for tests of genetic interactions, where the objective is to identify those genes that have a specific role in controlling the expression of insulin-like genes, or promoting the growth and differentiation of the tissues that expresses the insulin-like protein. Transgenic *Drosophila* carrying an insulin-like regulatory element-reporter gene fusion can be crossed with another *Drosophila* strain carrying a mutation-of-interest and the resulting progeny examined. For example, the mutation-of-interest might be a modifier mutation arising from a genetic modifier screen as described in a preceding section. If no change of expression of the reporter gene in the resulting progeny is observed, this is indicative of a lack of involvement of the gene altered by the mutation-of-interest in controlling insulin-like protein expression; by contrast, if a significant increase, decrease, loss, or mis-expression of the reporter protein in the resulting progeny is observed, this is indicative of a regulatory role for the gene altered by the mutation-of-interest in cells expressing the insulin-like protein.

Protein-DNA Binding Assays

In a third embodiment, insulin-like gene regulatory DNA elements are also useful in protein-DNA binding assays to identify gene regulatory proteins that control the expression of insulin-like genes. Such gene regulatory proteins can be detected using a variety of methods that probe specific protein-DNA interactions well known to those skilled in the art (Kingston, 1998, In *Current Protocols in Molecular Biology*, Ausubel et al, John Wiley & Sons, Inc., sections 12.0.3-12.10) including *in vivo* footprinting assays based on protection of DNA sequences from chemical and enzymatic modification within

living or permeabilized cells, *in vitro* footprinting assays based on protection of DNA sequences from chemical or enzymatic modification using protein extracts nitrocellulose filter-binding assays and gel electrophoresis mobility shift assays using radioactively labeled regulatory DNA elements mixed with protein extracts. In particular, it is of interest to identify those DNA binding proteins whose presence or absence is specific to insulin-like protein expressing tissue, as judged by comparison of the DNA-binding assays described above using cells/extracts from an insulin-like gene expressing tissue versus other cells/extracts from tissues that do not express insulin-like genes. For example, a DNA-binding activity that is specifically present in cells that normally express an insulin-like protein might function as a transcriptional activator of the insulin-like gene; conversely, a DNA-binding activity that is specifically absent in cells that normally express an insulin-like protein might function as a transcriptional repressor of the insulin-like gene. Having identified candidate insulin-like gene regulatory proteins using the above DNA-binding assays, these regulatory proteins can themselves be purified using a combination of conventional and DNA-affinity purification techniques. In this case, the DNA-affinity resins/beads are generated by covalent attachment to the resin of a small synthetic double stranded oligonucleotide corresponding to the recognition site of the DNA binding activity, or a small DNA fragment corresponding to the recognition site of the DNA binding activity, or a DNA segment containing tandemly iterated versions of the recognition site of the DNA binding activity. Alternatively, molecular cloning strategies can be used to identify proteins that specifically bind insulin-like gene regulatory DNA elements. For example, a *Drosophila* cDNA library in an *E. coli* expression vector, such as the lambda-gt11 vector, can be screened for *Drosophila* cDNAs that encode insulin-like gene regulatory element DNA-binding activity by probing the library with a labeled DNA fragment, or synthetic oligonucleotide, derived from the insulin-like gene regulatory DNA, preferably using a DNA region where specific protein binding has already been demonstrated with a protein-DNA binding assay described above (Singh et al., 1989, Biotechniques 7:252-61). Similarly, the yeast "one-hybrid" system can be used as another molecular cloning strategy (Li and Herskowitz, 1993, Science 262:1870-4; Luo, et al., 1996, Biotechniques 20(4):564-8; Vidal, et al., 1996, Proc. Natl. Acad. Sci. U.S.A. 93(19):10315-20). In this case, the insulin-like gene regulatory DNA element is operably fused as an upstream activating sequence (UAS) to one, or typically more, yeast reporter genes such as the *lacZ* gene, the *URA3* gene, the *LEU2* gene, the *HIS3* gene, or the *LYS2*

gene, and the reporter gene fusion construct(s) inserted into an appropriate yeast host strain. It is expected that in the engineered yeast host strain the reporter genes will not be transcriptionally active, for lack of a transcriptional activator protein to bind the UAS derived from the *Drosophila* insulin-like gene regulatory DNA. The engineered yeast host strain can be transformed with a library of *Drosophila* cDNAs inserted in a yeast activation domain fusion protein expression vector, e.g. pGAD, where the coding regions of the *Drosophila* cDNA inserts are fused to a functional yeast activation domain coding segment, such as those derived from the GAL4 or VP16 activators. Transformed yeast cells that acquire *Drosophila* cDNAs that encode proteins that bind the *Drosophila* insulin-like gene regulatory element can be identified based on the concerted activation the reporter genes, either by genetic selection for prototrophy (e.g. *LEU2*, *HIS3*, or *LYS2* reporters) or by screening with chromogenic substrates (*lacZ* reporter) by methods known in the art.

Use Of *Drosophila* Insulin-Like Proteins As A Media Supplement For Growth And Maintenance Of Insect Cells In Culture

Not all insect cells can be propagated effectively in available media and furthermore it is difficult and time consuming to wean cells onto serum-free media for large scale protein production. The present invention provides for the use of *Drosophila* homologs of insulin-like proteins, as media additive for growth and maintenance of cells in culture. Moreover, given that the *Drosophila* insulin-like proteins are the authentic endogenous protein hormones for *Drosophila* cells, and are likely to be more structurally and functionally similar to the authentic endogenous insulin-like hormones for other insect species, it is expected that *Drosophila* insulin-like hormones will exhibit superior properties in promoting growth and differentiation of insect cells in culture compared to the effects found for mammalian insulins on insect cells.

In a specific embodiment, the *Drosophila* insulin-like proteins are used for the in vitro cultivation of *Drosophila* or other insect cells. Insect cell lines are widely used for basic research on the cell and molecular biology of insects. Also, *Drosophila* and other insect cell lines have application as a preferred system for developing cell-based assays for insecticide targets, particularly those that might be amenable to high throughput screening methods (US Patent No. 5,767,261; US Patent No. 5,487,986; US Patent No. 5,641,652; US Patent No. 5,593,862; US Patent No. 5,593,864; US Patent No. 5,550,049; US Patent

No. 5,514,578).

In another embodiment, the *Drosophila* insulin-like proteins are employed for the *in vitro* cultivation of *Drosophila* and other insect cell lines used as host cells for the economical production of recombinant proteins on laboratory, pilot, or commercial scales.

Further, the *Drosophila* and other insect cell lines can be used as hosts for the large-scale growth *in vitro* of viruses or bacteria that can be used as commercial insect control agents

Although fetal calf serum has been traditionally used as a media additive for the growth of insect cells in culture, it has a number of serious disadvantages. First, fetal calf serum is expensive, and is often used in large amounts at concentrations typically between 5% to 15%. Occasionally, fetal calf serum is not available commercially. Also, there are batch-to-batch variations in the activity of fetal calf serum in stimulating cell growth, and some batches have been found to be toxic to insect cells in culture. Thus, there is a need for substitutes for fetal calf serum in growth media for insect cells in culture, and the use of *Drosophila* insulin-like proteins for this purpose is expected to help fulfill this need.

Accordingly, *Drosophila* insulin-like proteins described herein can be used as an additive to insect cell growth media at concentrations preferably ranging from 5 ng/L to 0.5 g/L, and as a substitute for either fetal calf serum or mammalian insulin, for the following purposes (a) promoting the propagation of continuous insect cell lines from primary cultures; (b) promoting the differentiation and maintenance of specific insect cell types in culture such as nerve cells, muscle cells, or fat body cells; (c) promoting the propagation of insect cell lines *in vitro* for use in cell-based pesticide screening assays; (d) promoting the propagation of insect cell lines *in vitro* for use in large-scale production of recombinant proteins, natural protein products, or other natural products; and (e) promoting the propagation of insect cells for the large-scale production of viruses and bacteria which use insect cells as a host.

Agricultural Uses Of *Drosophila* Insulin-Like Genes

In another embodiment of the invention, *Drosophila* insulin-like genes may be used in controlling agriculturally important pest species. For example, the proteins disclosed herein, or analogs or derivatives thereof, may have activity in modifying the growth, feeding and/or reproduction of crop-damaging insects, or insect pests of farm animals or of other animals. In general, effective pesticides exert a disabling activity on the target pest such as lethality, sterility, paralysis, blocked development, or cessation of

feeding. Examples of such pests include egg, larval, juvenile and adult forms of flies, mosquitos, fleas, moths, beetles, cicadia, grasshoppers, and crickets.

Tests for such activities can be any method known in the art. Pesticides comprising the nucleic acids of the *Drosophila* insulin like proteins may be prepared in a suitable vector for delivery to a plant or animal. Examples of such vectors include *Agrobacterium tumefaciens* Ti plasmid-based vectors for the generation of transgenic plants or recombinant cauliflower mosaic virus for the inoculation of plant cells or retrovirus based vectors for the introduction of genes into vertebrate animals (Burns et al., 1993, Proc. Natl. Acad. Sci. USA 90:8033-37); and vectors based on transposable elements for the introduction of genes into insects. For example, transgenic insects can be generated using a transgene comprising an insulin-like gene operably fused to an appropriate inducible promoter. For example, a tTA-responsive promoter may be used in order to direct expression of the insulin-like protein at an appropriate time in the life cycle of the insect. In this way, one may test efficacy as an insecticide in, for example, the larval phase of the life cycle (i.e. when feeding does the greatest damage to crops).

Further, recombinant or synthetic insulin-like proteins, analogs, or derivatives can be assayed for insecticidal activity by injection of solutions of insulin-like proteins into the hemolymph of insect larvae (Blackburn, et al., 1998, Appl. Environ. Microbiol. 64(8):3036-41; Bowen and Ensign, 1998, Appl. Environ. Microbiol. 64(8):3029-35). Still further, transgenic plants that express insulin-like proteins can be tested for activity against insect pests (Estruch, et al., 1997, Nat. Biotechnol. 15(2):137-41).

In a preferred embodiment, insulin-like genes can be tested as insect control agents in the form of recombinant viruses that direct the expression of an insulin-like gene in the target pest. Suitable recombinant virus systems for expression of proteins in infected insect cells include recombinant Semliki Forest virus (DiCiommo and Bremner, 1998, J. Biol. Chem. 273:18060-66), recombinant sindbis virus (Higgs et al., 1995, Insect Mol. Biol. 4:97-103; Seabaugh et al., 1998, Virology 243:99-112), recombinant pantropic retrovirus (Matsubara et al., 1996, Proc. Natl. Acad. Sci. USA 93:6181-85; Jordan et al., 1998, Insect Mol. Biol. 7:215-22), and most preferably recombinant baculovirus. The use of recombinant baculovirus has a number of specific advantages including host specificity, environmental safety, the availability of easily manipulable vector systems, and the potential use of the recombinant virus directly as a pesticide without the need for purification or formulation of the insulin-like protein. Thus, recombinant baculoviruses

that direct the expression of insulin-like genes can be used for both testing the pesticidal activity of insulin-like proteins under controlled laboratory conditions, and as insect control agents in the field. One disadvantage of wild type baculoviruses as insect control agents can be the amount of time between application of the virus and death of the target insect, typically one to two weeks. During this period, the insect larvae continue to feed and damage crops. Consequently, there is a need to develop improved baculovirus-derived insect control agents which result in a rapid cessation of feeding of infected target insects. The well-known metabolic regulatory role of insulins in vertebrates raises the possibility that expression of insulin-like proteins from recombinant baculovirus in infected insects may have a desirable effect in controlling metabolism and limiting feeding of insect pests.

Mutational analysis of insulin-like genes may also be used in connection with the control of agriculturally-important pests. In this regard, mutational analysis of genes encoding insulin-like hormones in *Drosophila* provides a rational approach to determine the precise biological function of this class of hormones in invertebrates. Further, mutational analysis provides a means to validate potential pesticide targets that are constituents of these signaling pathways.

Drosophila insulin-like genes, proteins or derivatives thereof may be formulated with any carrier suitable for agricultural use, such as water, organic solvents and/or inorganic solvents. The pesticide composition may be in the form of a solid or liquid composition and may be prepared by fundamental formulation processes including dissolving, mixing, milling, granulating, and dispersing.

The present invention encompasses compositions containing a *Drosophila* insulin-like protein or gene in a mixture with agriculturally acceptable excipients known in the art, such as vehicles, carriers, binders, UV blockers, adhesives, hemecants, thickeners, dispersing agents, preservatives and insect attractants. Thus the compositions of the invention may, for example, be formulated as a solid comprising the active agent and a finely divided solid carrier. Alternatively, the active agent may be contained in liquid compositions including dispersions, emulsions and suspensions thereof. Any suitable final formulation may be used, including for example, granules, powder, bait pellets (a solid composition containing the active agent and an insect attractant or food substance), microcapsules, water dispersible granules, emulsions and emulsified concentrates.

Examples of adjuvant or carriers suitable for use with the present invention include

water, organic solvent, inorganic solvent, talc, pyrophyllite, synthetic fine silica, attapugus clay, kieselguhr chalk, diatomaceous earth, lime, calcium carbonate, bontonite, fuller's earth, cottonseed hulls, wheat flour, soybean flour, pumice, tripoli, wood flour, walnut shell flour, redwood flour, and lignin.

- 5 The compositions of the present invention may also include conventional insecticidal agents and/or may be applied in conjunction with conventional insecticidal agents.

EXAMPLES

10

Identification Of *D. Melanogaster* Insulin-Like Genes

- A family of insulin-like genes has been identified in the model organism *D. melanogaster* (i.e., the fly *Drosophila melanogaster*). This invention provides the following examples of identification of three *Drosophila* insulin-like genes as illustrated in
15 the alignment of FIG. 8 and described in detail below.

Identification Of *Drosophila* Insulin-Like Genes In Genomic Sequence

- A *Drosophila* cDNA encoding an insulin-like protein, termed dIns1, was identified by random sequencing of cDNAs in a library enriched for sequences expressed in the
20 mesoderm (U.S. Patent Application Serial No. 09/201,226). We reasoned that other members of the insulin-like gene family in *Drosophila* could be identified by isolation and characterization of the genomic region surrounding the dINS1 gene.

- Sequence database searches using the BLAST revealed that the dIns1 cDNA was identical over a 217 bp region to Dm3500, a sequence tagged site (STS) mapped by the
25 Berkeley *Drosophila* Genome Project to chromosome 3, band 67C-D. Several P1 clones of genomic DNA had been molecularly mapped into a contig containing this STS, DS00060. Bacterial colonies containing P1 clones that molecularly map in and around DS00060 were obtained from Genome Systems, Inc. (St. Louis, Missouri). DNA from each of bacterial culture was screened for the presence of the dIns1 gene using a
30 PCR-based assay. A small sample from each colony was picked with the end of a toothpick and transferred directly into 15 μ l of PCR reaction buffer (supplied by the manufacturer, Perkin Elmer) containing 0.75 units Perkin Elmer Taq DNA polymerase, 2.5 mM MgCl₂, and 2.5 μ M each of the following DNA primers:

LepEco5: CTA GGA ATT CGA TCG AGC AGG ATG AG (SEQ ID NO:8)

LepXba3: CAC TTC TAG ATC ATC AGG CGC AGT AG (SEQ ID NO:9)

5 Thermocycling conditions used were as follows (where 0:00 indicates time in minutes:seconds): an initial denaturation of 94°C, 4:00 followed by 35 cycles of 95°C, 0:30; 55°C, 1:00; and 72°C, 0:45. Products of the PCR reactions were analyzed by agarose gel electrophoresis. One of the P1 clones from this library, DS05250 (well L11, plate 14), was confirmed to produce a PCR product of the expected size for dINS1 and
10 was selected for DNA sequencing.

The bacterial culture containing the DS05250 P1 clone was spread on an LB agar plate containing 25 µg/ml kanamycin, incubated overnight at 37°C, and a single colony was picked and used to inoculate 250 ml of Luria broth containing 25 µg/ml kanamycin. The culture was incubated with shaking at 37°C for 16 hours, bacterial cells were collected
15 by centrifugation, and DNA was purified with a Qiagen Maxi-Prep System kit (QIAGEN, Inc., Valencia, California). The entire DNA sequence of the DS05250 P1 insert was obtained using a strategy that combined shotgun and directed sequencing of a small insert plasmid DNA library derived from the DS05250 P1 DNA (Ruddy DA, et al. Genome Research, 1997, 7:441-456). All DNA sequencing reactions were performed using
20 standard protocols for the BigDye sequencing reagents (Applied Biosystems, Inc. Foster City, California) and products were analyzed using ABI 377 DNA sequencers. Trace data obtained from the ABI 377 DNA sequencers was analyzed and assembled into contigs comprising the complete P1 insert sequence using the phred-phrap computational package (Phil Green, U. of Washington).

25 **Computational Strategy**

The complete DNA sequence of the DS05250 P1 clone was analyzed by computational methods to identify insulin-like genes and other genes that might reside on this clone. The TBLASTN computer program (Altschul, et al., 1990, J. Mol. Biol.
30 215(3):403-10; Altschul, et al., 1997, Nucleic Acids Res. 25(17):3389-402) was employed with the dIns1 predicted protein sequence as a query to identify other insulin-like genes in this region. The results revealed that DS05250 contained part of the dIns1 coding region, as well as three other putative insulin-like genes in adjacent sequences (named dIns2,

dIns3, and dIns4; *see* FIG. 3). The GeneFinder (Phil Green, University of Washington) and GenScan programs (Burge and Karlin, 1997, J. Mol. Biol. 268(1):78-94) were used to predict coding regions, splice junctions, promoters, and poly(A) addition sites for each of the new insulin-like genes.

5 The presence of other gene sequences was investigated using the GeneFinder program, and also by analysis with the BLAST family of programs using the DS05250 sequence as a query against public and proprietary DNA and protein sequence databases. This analysis indicated that the DS05250 DNA contained additional genes distal to the dIns4 coding region with respect to the other insulin-like genes (FIG. 3); one region
10 exhibited perfect homology to an uncharacterized *Drosophila* EST, and a second region exhibited a high degree of coding sequence homology with vertebrate anion channel proteins. Thus, we operationally defined the domain of the insulin-like multigene cluster in the DS05250 sequence as an 10,149 bp region that extends from the dIns1 end of the DNA insert to the start of the region homologous with the uncharacterized EST.

15 Since it was determined that the DS05250 P1 clone insert ended within the dIns1 gene and did not contain the complete cluster of insulin-like genes, a pooling strategy was employed using the remaining P1 clones mapped to this region in an effort to extend the sequence of the dIns1 end of this cluster. Accordingly, the following P1 clones were picked, pooled, and DNA prepared from bacterial cultures for DNA sequencing as
20 described above for the DS05250 P1 clone: DS04166, DS07104, DS01000, DS06457, DS00683, DS00010, and DS00833. The same DNA sequencing strategy of combined shotgun and directed sequencing was employed on the pooled P1 clone DNA as that described above for the isolated DS0520 DNA. Individual sequence reads from the P1 pool were assembled with the DS05250 sequence contig using the phred-phrap
25 computational package. The P1 pool strategy was successful in extending the sequence of the insulin-like gene cluster by 4.77 kbp beyond the end of the DS05250 sequence. Computational analysis of this additional sequence using the TBLASTN, GeneFinder, and GenScan programs, as above, revealed that the additional sequence from the P1 pool contained the N-terminal coding region of the dIns1 gene, an intergenic region, and an
30 adjacent gene exhibiting homology to an uncharacterized *Drosophila* EST (*see* FIG. 3). Thus, we could define the limits of the cluster of repeated insulin-like genes in this genomic location as an 10,781 bp segment extending from the end of the sequences containing a predicted open reading frame with homology to the uncharacterized EST on

the dIns1 end of the cluster to the uncharacterized EST on the dIns3 end of the cluster (Fig. 4). An annotated sequence of the insulin multigene cluster in the DS05250 is presented in FIG. 4.

5 Isolation And Sequence Characterization Of Cdnas Corresponding To The *Drosophila* Insulin-Like Genes

The structure and expression of each new insulin-like gene predicted in the DS05250 genomic clone (dIns2, dIns3, and dIns4) was confirmed by either PCR amplification of inserts in *Drosophila* cDNA libraries, or reverse transcription of *Drosophila* mRNA and PCR amplification of the resulting cDNA (RT-PCR), as described below. For each gene, PCR primers were designed such that one primer annealed upstream of the predicted ATG codon, and the second primer annealed downstream of the predicted stop codon.

dIns2

15 The template source was a Canton S adult, oligo-dT- and random-primed cDNA library in the UniZap vector, purchased from Stratagene (Stratagene USA, LaJolla, California). Library DNA was diluted to a concentration of approximately 2 ng/ μ l before use. dIns2 cDNA was amplified by PCR, using a ClonTech Advantage cDNA PCR kit (CLONETECH Laboratories, Inc., Palo Alto, California) and the following primers:

20

fins2U70:	CTTCATCACTCATGGGCATCGAG	(SEQ ID NO:10)
fins2L515:	TGGGTAAATAGGTTTACGAGGTT	(SEQ ID NO:11)

25 The PCR reaction contained 1 μ l 10 X KlenTaq buffer, 1 μ l dNTPs, and 1 μ l KlenTaq enzyme mix, all as supplied by the manufacturer; to which was added 1 μ l (2 ng) template DNA, and primers to a final concentration of 0.2 μ M. Reaction conditions were as follows (where 0:00 indicates time in minutes:seconds): 95°C, 4:00, followed by 30 cycles of 95°C, 0:30; 55°C, 1:00; 68°C, 0:45.

30 Reaction products were analyzed by agarose gel electrophoresis, and a single major species was observed whose size matched that expected for the dIns2 cDNA (468 bp). The PCR product was isolated by electrophoresis in a 2% low melting point agarose gel stained with ethidium bromide, and the region of the gel containing the DNA was excised with a razor blade. Agarose was removed by digestion of the gel slice with β -agarase as

follows: incubation at 65°C for 10 min, addition of approximately 1/10 vol. 10x β -agarase buffer, brief incubation at 40°C, addition of 5 units β -agarase, and incubation for 1 h at 40°C. The sample was quickly frozen in a dry ice/ethanol bath, and the remaining agarose removed by centrifugation in a microcentrifuge for 15 min. The supernatant was decanted and DNA precipitated by addition of sodium acetate to 0.3 M final concentration, a small amount of glycogen as carrier, and 2 volumes isopropanol. The mixture was left at -20°C for 30 min, and DNA collected by centrifugation in a microcentrifuge for 15 minutes. The resulting DNA pellet was dried and suspended in 10 μ l TE buffer (10 mM Tris-HCl, pH 8.0, 1 mM EDTA).

The purified dIns2 cDNA PCR product was cloned by ligation into the vector pCRII using the InVitrogen TA Cloning Kit (Invitrogen Corp., Carlsbad, California; Brun, et al., 1991, DNA Seq. 1(5):285-9) with subsequent transformation of *E. coli*, following the manufacturers directions. Individual transformant colonies were screened for the presence of the desired insert using a PCR assay with the dIns2-specific PCR primers (*i.e.* SEQ ID NO:10 and SEQ ID NO:11) described above. Plasmid DNA was isolated from the resulting colonies using an alkaline lysis method, and the insert DNA was sequenced using the BigDye sequencing kit (Applied Biosystems, Inc. Foster City, California) with universal M13 forward and reverse sequencing primers. The resulting sequence obtained for dIns2 cDNA (FIG. 5) was in agreement with that predicted from the DS05250 genomic sequence. Shown in Figure 5 is the annotated sequence of dIns2, which contains a signal sequence followed by a B peptide, C peptide, and A peptide, as indicated by the heavy lines below the respective sequences.

dIns3

The template source was freshly synthesized first strand cDNA generated using oligo-dT purified mRNA from 5 day old third instar larvae. cDNA synthesis was primed with oligo-dT primer containing a NotI site obtained from LifeTechnologies. The single stranded cDNA was amplified by PCR, using the ClonTech Advantage cDNA PCR kit and the following primers designed from the predicted dIns3 genomic sequence:

fins3OU16: GCTTCCGATTAGTGGTATAAA (SEQ ID NO:12)

fins3OL584: TTCGTATGTATGTATGTATGTG (SEQ ID NO:13)

The PCR reaction contained 1 μ l 10 X KlenTaq buffer, 1 μ l dNTPs, and 1 μ l KlenTaq enzyme mix, all as supplied by the manufacturer; to which was added 0.5 μ l template DNA and primers at a final concentration of 0.2 μ M. Reaction conditions were as follows (where 0:00 indicates time in minutes:seconds): 95°C, 4:00, followed by 30 cycles of 95°C, 0:30; 55°C, 1:00; 68°C, 0:45.

The reaction products were analyzed by gel electrophoresis and a single major species of the size expected for dIns3 was observed. The dIns3 cDNA product was cloned into the vector pCRII as described above for dIns2.

The dIns3 cDNA inserts in pCRII clones were sequenced by PCR amplification of the insert DNA with either M13 forward and reverse primers, or fins3OU16 and fins3OL584 primers, followed by cycle-sequencing of the amplification products. The sequence determined for the dIns3 cDNA clones (FIG. 6) was in agreement with that predicted from the genomic sequence derived from the DS05250 P1 clone. Shown in Figure 6 is the annotated sequence of dIns3, which contains a signal sequence followed by a B peptide, C peptide, and A peptide, as indicated by the heavy lines below the respective sequences.

dIns4

Reverse transcription and PCR amplification were used to obtain dIns4 cDNA clones as described above for dIns3 except that the following primers were used:

fins4U5:	TAAACCCATAACCATGAGCAAGC	(SEQ ID NO:14)
fins4L516:	TCAGTTGGGGTCAATGATTTTCG	(SEQ ID NO:15)

A single major product of the expected size was observed following agarose gel electrophoresis and the resulting dIns4 cDNA was purified, cloned and sequenced as described above for dIns2. The sequence determined for the dIns4 cDNA clone (FIG. 7) was in agreement with that predicted from the genomic sequence derived from the DS05250 P1 clone. Shown in Figure 7 is the annotated sequence of dIns4, which contains a signal sequence followed by a B peptide, C peptide, and A peptide, as indicated by the heavy lines below the respective sequences.

Structural Features Of Drosophila Insulin-Like Genes And Proteins

The genomic organization of *Drosophila* insulin-like genes revealed in the DS05250 sequence can be viewed as two pairs of genes, dIns1/dIns2 and dIns3/dIns4, where the genes in each pair are arranged in tandem and oriented in the same direction, but where each pair of genes is oriented in the opposite direction and transcribed convergently (see FIG. 3). This implies that during the evolution of this multigene cluster an inversion occurred to create this arrangement, as opposed to the simplest model for the generation of a multigene array resulting solely from unequal cross-over, which would produce tandem genes all oriented in the same direction (Kondo, et al., 1996, J. Mol. Biol. 259:926-937; Smit, et al., 1998, Prog. Neurobiol. 54:35-54).

The sequence of the genomic region of DS05250 also reveals that three of the four *Drosophila* insulin-like genes, dIns1, dIns2, and dIns4, have intervening sequences that disrupt coding regions. It is notable that the position of the intervening sequence is at essentially the same location in each of these genes: within the C peptide coding sequences very near the junction with the B peptide coding sequences (FIG. 4). This same approximate position of an intervening sequence is also frequently found in vertebrate insulin-like genes, supporting an evolutionary relationship between *Drosophila* and vertebrate members of the insulin superfamily (Murray-Rust, et al., 1992, BioEssays 14:325-331; McRory and Sherwood, 1997, DNA and Cell Biology 16:939-949). The dIns3 gene does not appear to have an intervening sequence that disrupts the coding region of this gene. There is precedent for this situation in the form of the bombyxin genes of *Lepidoptera*, which all lack intervening sequences (Kondo, et al., 1996, J. Mol. Biol. 259:926-937).

Alignment of the predicted sequences of the *Drosophila* insulin-like proteins with other vertebrate and invertebrate members of the insulin superfamily demonstrates that the *Drosophila* proteins all contain the key structural features known to be important for promoting proper folding and processing of these preprohormones (FIG. 8). It is particularly notable that each of the *Drosophila* insulin-like proteins (dIns1, dIns2, dIns3 and dIns4) possesses a large C peptide of more than 30 amino acids flanked by dibasic residues, which are recognized by prohormone convertases during removal of the C peptide from the prohormone. Also, none of the *Drosophila* insulin-like proteins have a large C- terminal extension, such as found in the E peptide region of IGFs. Consequently, the overall organization of the *Drosophila* insulin-like proteins is similar to that of vertebrate insulins rather than that of vertebrate IGFs, although the possibility remains that

one or more *Drosophila* insulin-like proteins might have a growth-promoting function similar to that of vertebrate IGFs. This is of interest since it remains uncertain when the structure and function of IGFs diverged from insulins during metazoan evolution (McRory and Sherwood, 1997, DNA and Cell Biology 16:939-949). Also, the *Drosophila*

5 insulin-like receptor InR exhibits a ligand-specificity with a preference for insulins as opposed to IGFs, even though InR appears to mediate growth-promoting activities in vivo.

All of the *Drosophila* insulin-like proteins possess exactly the same number (six) and spacing of Cys residues as found in vertebrate insulin superfamily proteins (boxed in FIG. 8), indicating that the disulfide bonding pattern stabilizing the folded structure of

10 these proteins would also be identical. This contrasts with the situation for some other invertebrate insulin-like proteins which have been found to have unusual disulfide features including an extra pair of Cys residues (represented in FIG. 8 by MIP-I from freshwater snail, and F13B12 from the nematode *C. elegans*) or which may lack the conserved Cys residues (Brousseau, et al., 1998, Early 1998 East Coast Worm Meeting, abstract 20;

15 Duret, et al., 1998, Genome Res. 8(4):348-53; Wisotzkey and Liu, 1998, Early 1998 East Coast Worm Meeting, abstract 206; Pierce and Ruvkun, 1998, Early 1998 East Coast Worm Meeting, abstract 150), or have altered spacing between Cys residues in the A or B chains (found in some *C. elegans* insulin-like proteins, (Kondo, et al., 1996, J. Mol. Biol. 259:926- 937; Smit, et al., 1998, Prog. Neurobiol. 54:35-54). It is also evident that all of

20 the *Drosophila* insulin-like proteins have hydrophobic residues in positions that normally contribute to stabilizing the core structure at the interface between the A and B peptides in the folded protein (shaded in FIG. 8). Given the presence of these conserved structural features in each of the *Drosophila* insulin-like proteins it is expected that they will adopt a secondary and tertiary structure very similar to that found in their vertebrate and

25 invertebrate counterparts, specifically a long central helix in the B peptide and two short antiparallel helices in the A peptide joined by a loop.

Despite the presence of such conserved structural features, phylogenetic analyses indicate that the *Drosophila* insulin-like proteins are rather diverse at the primary sequence level, particularly at positions expected to be exposed on the surface of the mature

30 hormones. This is all the more surprising given that these *Drosophila* genes are located immediately next to one another in the genome, and might therefore be expected to have evolved relatively recently from each other. By contrast, the very large family of known bombyxin proteins in *Lepidoptera* exhibits considerably less sequence divergence than the

family of four *Drosophila* insulin-like proteins discussed here. Similarly, the family of five insulin-like proteins found in the freshwater snail, the MIPS, are also less diverse at the protein sequence level than the four *Drosophila* insulin-like proteins. Indeed, the *Drosophila* insulin-like proteins are more divergent from each other than the degree of sequence divergence observed between vertebrate insulins and IGFs. Accordingly, this sequence divergence among the *Drosophila* insulin-like proteins suggests the possibility that they may serve distinctly different functions and/or act by binding through different receptor proteins.

10 Cross-Hybridization Experiment For dIns1, dIns2, dIns3, and dIns4

Sequence alignments of the four *Drosophila* insulin-like proteins revealed diversity among these family members at the amino acid level (see Fig. 8). Computational comparisons of the nucleic acid sequences using BLASTN and dot plot programs provided further evidence of sequence divergence in both coding and non-coding regions. As an experimental demonstration of the sequence divergence of the dIns1 genes, a Southern blotting experiment was performed where the dIns1 cDNA was used as probe to test cross-hybridization with the other *Drosophila* insulin-like genes, and a *C. elegans* insulin-like gene (F13B12), under conditions of low, medium, and high stringency, as described below.

20 Plasmid DNAs (0.5 g) containing inserts of each insulin-like cDNA were digested with an appropriate restriction enzyme to liberate the cDNA insert from the vector as follows: pcDNA3.1-dIns1, PmeI; pBS+-dIns2, EcoRI, pBS+-dIns3, EcoRI, pBS+-dIns4, EcoRI; and pcDNA3.1-F13B12, PmeI. The restriction enzyme digestions were divided into thirds (for testing low, medium and high stringency hybridization), arranged in three identical sets, and the products were separated by electrophoresis in a 1% agarose gel along with DNA size markers. DNA fragments were visualized by staining with ethidium bromide, UV transillumination, and photography. The results demonstrated complete digestion of each plasmid DNA, and importantly showed that approximately the same amount of each insulin-like cDNA fragment was present in the gel. DNAs in the gel were denatured by treatment with a 0.4 N NaOH solution, blotted to a Hybond N+ membrane (Amersham) by transfer in the same solution, and the membrane neutralized by washing in a buffer containing 0.5 M Tris-HCl, pH 7.2, 1 M NaCl. The membrane was cut into thirds, each containing an identical set of the different insulin-like cDNAs, and the

membranes were pretreated in a hybridization buffer (0.5 M sodium phosphate, pH 7.2, 7% SDS, 1 mM EDTA, and 1% bovine serum albumin) which also contained 100 g/ml sheared, denatured salmon sperm DNA. A DNA probe was prepared by digestion of a plasmid vector containing dIns1 cDNA with EcoRI to release the insert, separation of the dIns1 cDNA from the vector by agarose gel electrophoresis, and radiolabelling using ^{32}P -dCTP with an Amersham Rediprime DNA labelling kit following the manufacturers directions (final incorporation of radioactivity into the probe was 30 Ci). Hybridization of the probe to membranes was carried out by incubating each membrane in the hybridization buffer above along with 10 Ci of ^{32}P -labeled dIns1 cDNA probe overnight at 45°C. After hybridization, each membrane was washed two times each for 30 minutes each at 45°C in wash buffer #1 (40 mM sodium phosphate, pH 7.2, 5% SDS, 1 mM EDTA, 0.5% bovine serum albumin), followed by four washes each for 30 minutes in wash buffer #2 (40 mM sodium phosphate, pH 7.2, 1% SDS, 1 mM EDTA), and subsequently each membrane was treated differently as described below for low, medium, or high stringency hybridization conditions. For low stringency hybridization, one membrane was not washed further. For medium stringency hybridization, a second membrane was subjected to four washes each for 30 minutes in wash buffer #2 at 55°C. For high stringency hybridization, a third membrane was subjected to four washes each for 30 minutes in wash buffer #2 at 55°C, followed by four washes each for 30 minutes in wash buffer #2 at 65°C. The membranes were dried and radioactivity detected by autoradiography using X-ray film and an intensifying screen. Hybridization of the ^{32}P -labeled dIns1 cDNA probe to the homologous dIns1 cDNA on the membranes was readily detected after only 15 minutes of autoradiography under all three hybridization conditions, and increasing the time of autoradiography to 2.5 hours revealed no detectable cross-hybridization of dIns1 probe to the dIns2, dIns3, dIns4, or F13B12 cDNAs on the membranes under any hybridization condition. After 2.5 hours of autoradiography, very weak hybridization of the probe could be detected to pBS+ vector fragments and marker DNA fragments, which was most evident on the low and medium stringency membranes (presumably due to weak nonspecific hybridization). Thus, these results clearly demonstrate that there is no significant cross-hybridization of dIns1 cDNA to any of the other *Drosophila* insulin-like cDNAs, dIns2, dIns3, and dIns4, under conditions of either low, medium or high stringency. Furthermore, these results provide clear experimental evidence of the significant sequence divergence of these genes.

WHAT IS CLAIMED IS:

1. A purified protein comprising an amino acid sequence of an A peptide domain and/or B peptide domain of a *Drosophila* insulin-like protein selected from dIns2, dIns3 and dIns4, as depicted in Figure 8.

5

2. The purified protein of claim 1 comprising an amino acid sequence selected from any one of SEQ ID Nos 2, 4, and 6 and 8.

3. A purified antibody, or derivative thereof containing the idiotype of the antibody, capable of immunospecific binding to the protein of Claim 1 and not to an insulin-like protein of another species.

10

4. An isolated nucleic acid comprising a nucleotide sequence encoding an amino acid sequence as depicted in Figure 5 (SEQ ID NO:2), Figure 6 (SEQ ID NO:4), or Figure 7 (SEQ ID NO:6), wherein said nucleic acid is less than 15 kilobases.

15

5. The isolated nucleic acid of Claim 4 comprising a nucleotide sequence selected from SEQ ID NO: 1, 3, and 5.

20

6. A recombinant cell containing a recombinant nucleic acid vector comprising a nucleotide sequence encoding an amino acid sequence as depicted in Figure 5 (SEQ ID NO:2), Figure 6 (SEQ ID NO:4), or Figure 7 (SEQ ID NO:6).

25

7. A method of identifying a phenotype associated with mutation or abnormal expression of a *D. melanogaster* insulin-like protein comprising identifying an effect of a mutated or abnormally expressed *D. melanogaster* insulin-like gene which encodes a *D. melanogaster* insulin-like protein comprising an amino acid sequence as depicted in Figure 5 (SEQ ID NO:2), Figure 6 (SEQ ID NO:4), or Figure 7 (SEQ ID NO:6), in a *D. melanogaster* animal.

30

8. The method of Claim 7 wherein the gene is mutated or abnormally expressed using a technique selected from the group consisting of radiation mutagenesis, chemical mutagenesis, transposon mutagenesis, antisense and double-stranded RNA interference.

9. A modified, isolated *D. melanogaster* animal in which a *D. melanogaster* insulin-like gene which encodes a *D. melanogaster* insulin-like protein comprising an amino acid sequence as depicted in Figure 5 (SEQ ID NO:2), Figure 6 (SEQ ID NO:4), or
5 Figure 7 (SEQ ID NO:6) which has been deleted or inactivated by recombinant methods, or a progeny thereof containing the deleted or inactivated gene.

10. A recombinant non-human animal containing a *D. melanogaster* insulin-like transgene which encodes a *D. melanogaster* insulin-like protein comprising an amino acid
10 sequence as depicted in Figure 5 (SEQ ID NO:2), Figure 6 (SEQ ID NO:4), or Figure 7 (SEQ ID NO:6).

11. A method of identifying a molecule that alters the expression level of a *D. melanogaster* insulin-like gene corresponding to a cDNA sequence as depicted in Figure 5
15 (SEQ ID NO:1), Figure 6 (SEQ ID NO:3), or Figure 7 (SEQ ID NO:5), which method comprises:

(a) contacting a transgenic fly cell with one or more molecules, said transgenic fly cell having a transgene comprising a promoter or enhancer region of genomic DNA from 1 base to 6 kilobases upstream of the start codon of the cDNA sequence operably linked to a
20 reporter gene; and

(b) determining whether the level of expression of the reporter gene is altered relative to the level of expression of the reporter gene in the absence of the one or more molecules.

12. A cell culture medium or medium supplement comprising (a) a sterile liquid
25 carrier, and (b) a protein or fragment thereof, functional in promoting cell growth, survival, or differentiation, said protein comprising at least 10 contiguous amino acids as depicted in Figure 5 (SEQ ID NO:2), Figure 6 (SEQ ID NO:4), or Figure 7 (SEQ ID NO:6).

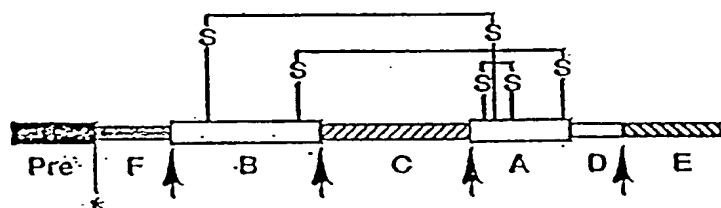


FIG. 1

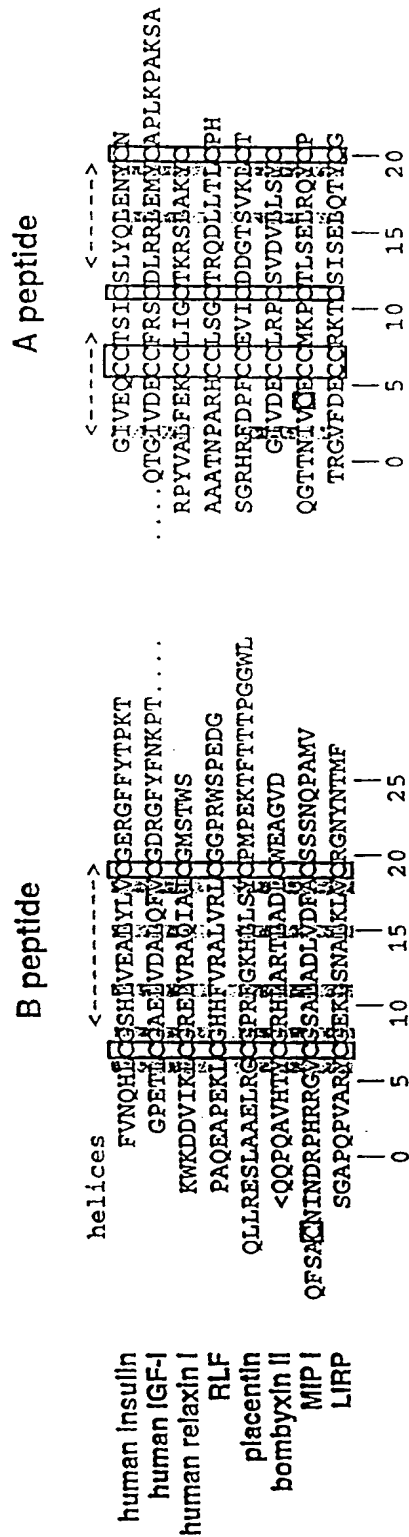


FIG. 2

Gene Map of *Drosophila* Insulin-like Gene Cluster Region

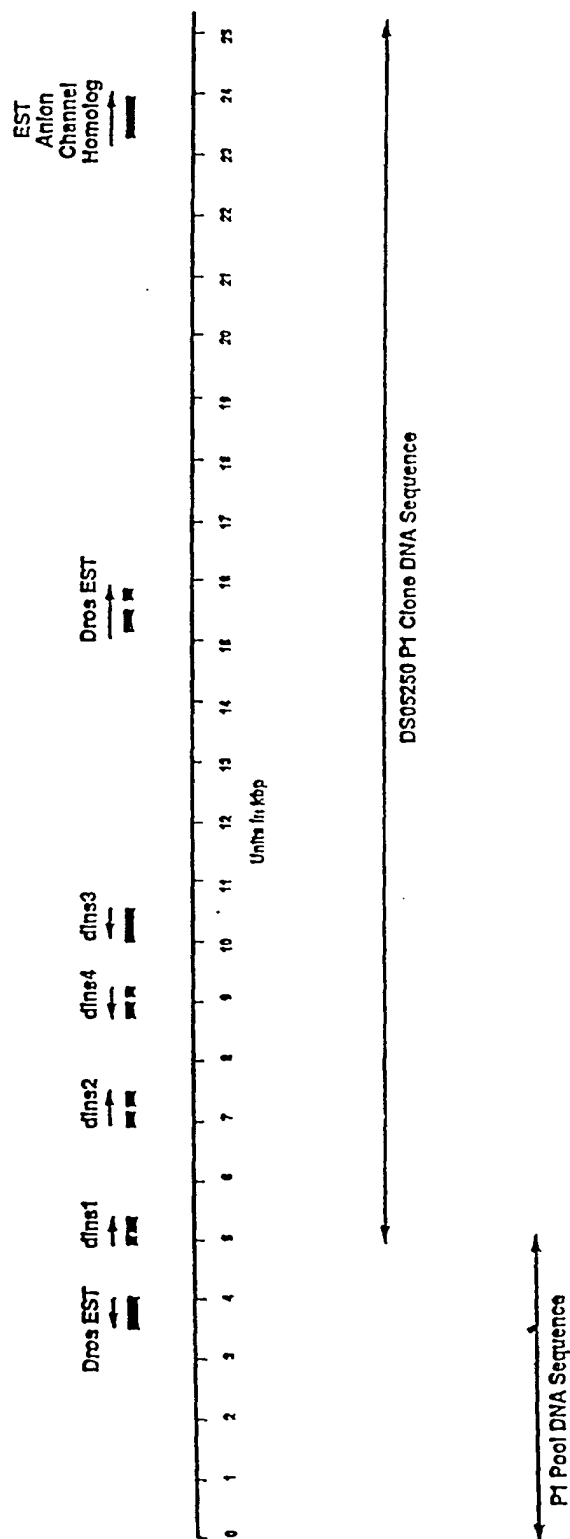


FIG. 3

Drosophila Insulin-like Gene Cluster Genomic DNA Sequence

```

      10      20      30      40      50      60
GCTTCTGCTCGGAGAGCGGCTGACCCGAATGGGATAGGGCATCTCCTGTCCACAGGAACG
CGAAGACGAGCCTCTCGCCGACTGGGCTTACCCTATCCCGTAGAGGACAGGTGTCCTTGC

      70      80      90     100     110     120
AACTCCCCATTATCGCCCTGCTTGGCCTTCATCGTCTTCACCGCCGATTCAATCAGTCTC
TTGAGGGGTAATAGCGGGACGAACCGGAAGTAGCAGAAAGTGGCGGCTAAGTTAGTCAGAG

     130     140     150     160     170     180
CAAGGACTATCGCAGTTGTAGTGTCCAAAGGGACCAGGTGGCTCCGATGCCGCACTATTG
GTTCTTGATAGCGTCAACATCACAGGTTTCCCTGGTCCACCGAGGCTACGGCGTGATAAC

     190     200     210     220     230     240
GCATTGGAGCCGGAACCGATCGTGCTAACTCCAGCAGCTTCTGTATATGTCCGCCCTGC
CGTAACCTCGGCCTTTGGCTAGCACGATTGAGGGTCGTGCAAGACATATACAGCGGGACG

     250     260     270     280     290     300
GTGGAGTAGAGTGTGTCAAGGTGGAGGTCACTAATGTGCCAGAAGTAGCCTGTCAACAAA
CACCTCATCTCACACAGTTCCACCTCCAGTGATTACACGGTCTTCATCGGACAGTTGTTT

     310     320     330     340     350     360
CAAGTAGAATCAAGTAAATGTGTTAGTTAAATACCCATAGATATATGTAAAAGTTGTTGT
GTTTCATCTTAGTTCATTTACACAATCAATTTATGGGTATCTATATACATTTTCAACAACA

     370     380     390     400     410     420
TTTATTTTGCTAAGAAAAGTTTAATCTATATCCCAGTTTACACACCAGATTTTATGTCC
AAATAAACGATTCTTTTCAAATTAGATATAGGGTCAAAATGTGTGGTCTAAAAATACAGG

     430     440     450     460     470     480
TGAGCAATTTTCGTATGTATTTCCCTTCGTAAAGTAAGGATCGAGATTAGACTTTGACTT
ACTCGTTAAAGCATAACATAAAGGGGAAGCATTTTCATTCCTAGCTCTAATCTGAAACTGAA

     490     500     510     520     530     540
TGGTTAAGTCGGGCAATTCCCTGGCCGGGAAAGGCCATTTCCCTTCGCGGGGCATTTTCCC
ACCAATTCAGCCCGTTAAGGACCGGCCCTTTCCGGTAAAGGAAAGCGCCCCGTAAAAGGG

     550     560     570     580     590     600
GCCGGCTGGTCGAGCGACAAAAATAAGAAAAACCTGGTAGTTCAAATGGAAATCTCCTGC
CGGCCGACCAGCTCGCTGTTTTTATTCTTTTTGGACCATCAAGTTTACCTTTAGAGGACG

     610     620     630     640     650     660
AGCTGACTGTTTGGTTGGTTGACTGACCTGGCCCGAATTTAACTTTCTACCTGGTCGCAA
TCGACTGACAAACCAACCAACTGACTGGACCGGGCTTAAATTGAAAGATGGACCAGCGTT

     670     680     690     700     710     720
TACGTGAAGTCAAAAAGTCAATTAGCGAGTCAACATTTTGAGCGCCGGCCAACTCCAAGG
ATGCACTTCAGTTTTTTCAGTTAATCGCTCAGTTGTAAAACTCGCGGCCGGTTGAGGTTCC
_____DINS1 PUT. PROMOTER_____>

```

FIG. 4A

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730 740 750 760 770 780
 ATCAGTATCATTGTCATGCCCAGCGATCGGTTTGCCAAGAGCACGAGAAGTTGAGATA
 TAGTCATAGTAAACCGTACGGGTGCTAGCCAAACGGTTCTCGTGCTCTTCAAGCTCTAT
 _____>

790 800 810 820 830 840
 GGACCCAGAGATACCAGAGATAAAGGAGGCATACCTTTTATGCCCGGTGAGAGCACGGAC
 CCTGGGTCTCTATGGTCTCTATTTCTCCGTATGGAAAATACGGGCCACTCTCGTGCCCTG

850 860 870 880 890 900
 GGCGGAGTGAAAGATCGAGCAGGATGAGCCTGATTAGACTGGGACTGGCGCTGCTGCTCC
 CCGCCTCACTTTCTAGCTCGTCCCTACTCGGACTAATCTGACCCTGACCGGACGACGAGG
 M S L I R L G L A L L L>
 _____DINS1 CODING REGION (EXON 1)_____>

910 920 930 940 950 960
 TGCTGGCCACCGTGTGCGCAGTTACTGCGAGCCGGTCCAGGGACGCCGAAAGATGTGCGGCG
 ACGACCGGTGGCACAGCGTCAATGACGTGCGCCAGGTCCCTGCGGCTTTCTACACGCCGC
 L L A T V S Q L L Q P V Q G R R K M C G>
 _____DINS1 CODING REGION (EXON 1)_____>

>End_of_DS05250_sequence

970 980 990 1000 1010 1020
 AGGCTCTGATCCAGGCACTGGATGTGATTTGTGTTAATGGATTTACACGCCGTGTCAGGC
 TCCGAGACTAGGTCCGTGACCTACACTAAACACAATTACCTAAATGTGCGGCACAGTCCG
 E A L I Q A L D V I C V N G F T R R V R>
 _____DINS1 CODING REGION (EXON 1)_____>

1030 1040 1050 1060 1070 1080
 GGAGCAGTGGTAAGTTTGGGTACTATGCATATTCGATTGGCTTCCATACATCTAACTTCT
 CCTCGTCACCATTCAAACCCATGATACGTATAAGCTAACCGAAGGTATGTAGATTGAAGA
 R S S A>
 _____>

1090 1100 1110 1120 1130 1140
 TTTGACAAGCGTCTAAGGATGCTAGAGTGCGAGACCTTATCCGTAAGCTACAGCAGCCG
 AAAGCTGTTTCGCAGATTCTACGATCTCAGCTCTGGAATAGGCATTGATGTGCTCGGC
 S K D A R V R D L I R K L Q Q P>
 _____DINS1 CODING REGION (EXON-2)_____>

1150 1160 1170 1180 1190 1200
 GATGAGGACATTGAACAGGAAACGGAAACGGGAAGGTTAAAGCAGAAGCATAACGGATGCG
 CTACTCCTGTAACTTGTCTTTGCTTTGCCCTTCCAATTTCTGCTTCTGATGCTTACGC
 D E D I E Q E T E T G R L K Q K H T D A>
 _____DINS1 CODING REGION (EXON-2)_____>

1210 1220 1230 1240 1250 1260
 GATACGGAGAAGGGTGTGCCACCGGCCGTGCGAAGTGGACGAAAGTTGCGACGCCATCGG
 CTATGCCTCTTCCACACGGTGGCCGGCAGCCTTCACCTGCTTTCAACGCTGCGGTAGCC
 D T E K G V P P A V G S G R K L R R H R>
 _____DINS1 CODING REGION (EXON-2)_____>

FIG. 4B

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      1270      1280      1290      1300      1310      1320
CGACGCATCGCCACGAGTGTTCGAAGGAGGGCTGCACCTACGACGATATACTGGACTAC
GCTGCGTAGCGGGTGCTCACAACGTTCCCTCCCGACGTGGATGCTGCTATATGACCTGATG
R  R  I  A  H  E  C  C  K  E  G  C  T  Y  D  D  I  L  D  Y>
_____DINS1 CODING REGION (EXON-2)_____>

                                >dIns1_poly(A)_signal
                                |
      1330      1340      1350      1360      1370      1380
TGCGCCTGATGACCAGGATGGCAAAACAAAACAAATAAAAACCAGAAACCAGATCCCAAA
ACGCGGACTACTGGTCCTACCGTTTTGTTTTGTTTATTTTTGGTCTTTGGTCTAGGGTTT
C  A  *>
_____>

      1390      1400      1410      1420      1430      1440
AACCAAGTACCAGATGAACACGACATGGCTGAGATTTTGTGTGGCGGCACGGGGAAAACA
TTGGTTCATGGTCTACTTGTGCTGTACCGACTCTAAACACACCGCCGTGCCCCTTTTGT

      1450      1460      1470      1480      1490      1500
CCCAGCGACCGGCAGGCTATTTGCAATTCATTTTCTACTACACTTAACCCCTAACTATA
GGGCTGCTGGCCGTCCGATAAACGTTAAGTAAAAGGATGATGTGAATTGGGGATTGATAT

      1510      1520      1530      1540      1550      1560
AACGTAATCGTATTTCCAAATATTTTCAATTGTAAAATTTCTAGTGGAGGCAAATAAGTTA
TTGCATTAGCATAAAGGTTTATAAAGTAACATTTTAAAGATCACCTCCGTTTATTTCAAT

      1570      1580      1590      1600      1610      1620
CTCTCCAAGCAGCAGCAGAAACAAAAGAAGAGTCCATTGCTTTTTTCTACATTCTACGCC
GAGAGGTTTCGTTCGTCTTTGTTTTCTTCTCAGGTAACGAAAAAAGATGTAAGATGCGG

      1630      1640      1650      1660      1670      1680
CTGCAGCATTCAGCTGTGAGGCATGGGGAATCCCCCTTGTATTCAAACCACCCGAAGCC
GACGTTCGTAAGGTCGACACTCCGTACCCCTTAGGGGAACAATAAGTTTGGTGGGCTTCGG

      1690      1700      1710      1720      1730      1740
ACCCAAACCATCGAGCCACCCACAAGCAGCTGCCATTTCAGCACCTCGAGTGCGGTGCCCT
TGGGTTTGGTAGCTCGGTGGGTGTTTCGTGACGGTAAGTCGTGGAGCTCACGCCACGGGA

      1750      1760      1770      1780      1790      1800
TGTTTTCCGAGAACAAATAATGAAAAATATGAATTTTAAATTAGATGACGTTCTGATTTTA
ACAAAAGGCTCTTGTTATTACTTTTATACTTAAAAATTAATCTACTGCAAGACTAAAAT

      1810      1820      1830      1840      1850      1860
ATAAGCAAAACAAAAGGTGGAGACAAAACGAACTCGGTAATACACTCAGATTGGAATTTA
TATTCGTTTTGTTTTCCACCTCTGTTTTGCTTGAGCCATTATGTGAGTCTAAGCTTAAAT

      1870      1880      1890      1900      1910      1920
CAGCTTCCTTTTTATCCATAATTTTTGTTATTATCGAAGGAGCGATATCAAACTAGAAA
GTCGAAGGAAAAATAGGTATTAAAAACAATAATAGCTTCCTCGCTATAGTTTTGATCTTT

      1930      1940      1950      1960      1970      1980
ACAACTTCCAATCAGTAGCGGGATTTTCCGAAGATAACACTCTATTCAACCGAAGGGTTT
TGTTGAAGGTTAGTCATCGCCCTAAAAGGCTTCTATTGTGAGATAAGTTGGCTTCCCAA
```

FIG. 4C

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1990 2000 2010 2020 2030 2040
TGAAATGATAATAATTCCGTTCTTACAGGTAAAAATCTATACTAATACCTGTTTTTTTGC
ACTTTACTATTATTAAGGCAAGAATGTCCATTTTGTAGATATGATTATGGACAAAAAACG

2050 2060 2070 2080 2090 2100
GGACGGAAAAAAGGCTCAGTTGGCTTATCATTTGGCAAAGGGACTTGGGGAAACCATAAA
CCTGCCTTTTTTCCGAGTCAACCGAATAGTAACCGTTTTCCCTGAACCCCTTTGGTATTT

2110 2120 2130 2140 2150 2160
GTATCGAAGGTACTGAGCCAAGATAATGAGATAACAGAAGGCGACTTTATTGTTTCCAC
CATAGCTTCCATGACTCGGTTCTATTACTCTATTGTCTTCCGCTGAAATAACAAAAGGTG

2170 2180 2190 2200 2210 2220
TCAAAAGCAATTGAATAAGTTGGCACTCGTTTMTAATTGAATGGGAATGAAATAAGCTCT
AGTTTTCGTTAACTTATTCAACCGTGAGCAAAAATTAACCTACCCCTACTTTATTTCGAGA

2230 2240 2250 2260 2270 2280
AAAAGTGTGTGTTAAACGTAATGGCTTTTGTGTTAATTTAAAGAATTTAAGTAGTTTTGA
TTTTACACAACAATTTTGCATTACCGAAAAACACAATTAAATTTCTTAAATTCATCAAAACT

2290 2300 2310 2320 2330 2340
AAGTATCATTTATTCTTTAGGTAATTTTATTACATTCCAAATTTAATAAATGACTAATTC
TTCATAGTAATAAGAAATCCATTAAAAATAATGTAAGGTTTAAATTATTTACTGATTAAG

2350 2360 2370 2380 2390 2400
GAAAAAGTGTTTATTTAATCAATGAATATATTTCAAGTAAGTTTACTTTTAGTAGCTTGC
CTTTTTACAAAATAAATTAGTTACTTATATAAAGTTCATTCAAATGAAATCATCGAACG

2410 2420 2430 2440 2450 2460
CAAATGTGAGTTTAAATATGTATGCATAGAACTATATAGTTAAACTGCTAAACTTTACAG
GTTTACACTCAAATTTATACATACGTATCTTGATATATCAATTTGACGATTTGAAATGTC

2470 2480 2490 2500 2510 2520
TTAAACTTTCTGAACCCACCAAAATGGATGAACATCCTCGTCTGCCGAAGGGAACTCGAT
AATTTGAAAGACTTGGGTGGTTTTACCTACTTGTAGGAGCAGACGGCTTCCCTTGAGCTA

2530 2540 2550 2560 2570 2580
GCACGTCATTTTGTTTTTCAACAATCCAGATCCGTGCGCTACTCCTTGGGCGAGAAAGTA
CGTGCAGTAAACAAAAAGTTGTTAGGTCTAGGCACGCGATGAGGAACCCGCTCTTTCAT

2590 2600 2610 2620 2630 2640
AACAAACGCCAGCTGATATGCGTCAGACCCCCCGGGCTCATCATCATCTCACCATTTTCAG
TTGTTTGCGGTGCGACTATACGCAGTCTGGGGGGCCCGAGTAGTAGTAGAGTGGTAAAGTC

2650 2660 2670 2680 2690 2700
ACATCCCATGCCAGCCCGAATCCTCAAGAGAACTAGACCAGACCAGGGCGACTACATA
TGTAGGGTACGGTCCGGCTTAGGAGTGCTCTTTGATCTGGTCTGGTCCCGCTTGATGTAT

2710 2720 2730 2740 2750 2760
TGTGGATGATGCTAACTGACACTACGGCTGACTCATGCTGACAGTGCTCAGACGCTGGAT
ACACCTACTACGATTGACTGTGATGCCGACTGAGTACGACTGTACAGAGTCTGCGACCTA

FIG. 4D

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2770 2780 2790 2800 2810 2820
ACAGCCCGCAGACATCCAACTCGTATCCTATCCGATTCTGCCCCATATATATAACCCCTCA
TGTCGGGCGTCTGTAGGTTGAGCATAGGATAGGCTAAGACGGGGTATATATATTGGGAGT
____DINS2 PUT. ____>

2830 2840 2850 2860 2870 2880
GTCGATGGCTGGGAGGCAAACAGTTGAGGCCGTGCCACTTGGCAGACACATACTACACAC
CAGCTACCGACCCTCCGTTTGTCAACTCCGGCACGGTGAACCGTCTGTGTATGATGTGTG
____DINS2 PUT. PROM____>

2890 2900 2910 2920 2930 2940
TCCCCGGGGGATTACGCATCCATACTTAAACACCACTTCATCACTCATGGGCATCGAGA
AGGGGCCCCCTAAGTGCGTAGGTATGAATTTGTGGTGAAGTAGTGAGTACCCGTAGCTCT
____>

2950 2960 2970 2980 2990 3000
TGAGGTGTCAGGACAGGAGGATCCTGCTACCTAGCCTACTCCTACTAATCCTTATGATCG
ACTCCACAGTCCTGTCTCCTAGGACGATGGATCGGATGAGGATGATTAGGAATACTAGC
M R C Q D R R I L L P S L L L L I L M I>
____DINS2 CODING REGION (EXON-1)____>

3010 3020 3030 3040 3050 3060
GCGGTGTCCAGGCCACCATGAAGTTGTGCGGCCGCAAACCTGCCCGAAACTCTCTCCAAGC
CGCCACAGGTCCGGTGGTACTTCAACACGCCGGCGTTTGACGGGCTTTGAGAGAGGTTCCG
G G V Q A T M K L C G R K L P E T L S K>
____DINS2 CODING REGION (EXON-1)____>

3070 3080 3090 3100 3110 3120
TCTGTGTGTATGGCTTCAACGCAATGACCAAGAGAACTTTGGGTAGGTGGGATTTTCTT
AGACACACATACCGAAGTTGCGTTACTGGTTCTCTTGAAACCCATCCACCCTAAAAAGAA
L C V Y G F N A M T K R T L D>
____DINS2 CODING REGION (EXON-1)____>

3130 3140 3150 3160 3170 3180
GATATAAGGAATACTAAAGTGCCATATCTCTTTACTTTTACCTAACACCTGTAGACCCCG
CTATATTCCTTATGATTTACGGTATAGAGAAATGAAAGTGGATTGTGGACATCTGGGGC
P>
____>

3190 3200 3210 3220 3230 3240
TGAACCTCAATCAGATCGATGGCTTGAAGACCGTTCCCTGCTGGAAAGACTGTTGAGTG
ACTTGAAGTTAGTCTAGCTACCGAAGCTTCTGGCAAGGGACGACCTTTCTGACAACCTCAC
V N F N Q I D G F E D R S L L E R L L S>
____DINS2 CODING REGION (EXON-2)____>

3250 3260 3270 3280 3290 3300
ATAGTTCCGGTTCAGATGCTCAAGACTCGACGTCTTCGGGATGGAGTCTTCGACGAGTGTT
TATCAAGCCAAGTCTACGAGTTCTGAGCTGCAGAAGCCCTACCTCAGAAGCTGCTCACAA
D S S V Q M L K T R R L R D G V F D E C>
____DINS2 CODING REGION (EXON-2)____>

FIG. 4E

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3310 3320 3330 3340 3350 3360
GCCTGAAGTCGTGCACCATGGATGAGGTGCTGAGATATTGTGCTGCCAAGCCGAGAACGT
CGGACTTCAGCACGTGGTACCTACTCCACGACTCTATAACACGACGGTTCGGCTCTTGCA
C L K S C T M D E V L R Y C A A K P R T>
_____DINS2 CODING REGION (EXON-2)_____>

3370 3380 3390 3400 3410 3420
AAACCTCGTAAACCTATTAACCCAATGACGACAACCTGCGATGATTGAAATGGAATGAAAG
TTTGGAGCATTTGGATAATTGGGTACTGCTGTTGACGCTACTAACTTTACCTTACTTTC
*>
____>

3430 3440 3450 3460 3470 3480
GACCCGATTGGGGAAAGCACTCACGTAATCATAGTTGTTAAGTCGTTATCGAAGCCTACT
CTGGGCTAACCCCTTTCGTGAGTGCAATTAGTATCAACAATTCAGCAATAGCTTCCGATGA

3490 3500 3510 3520 3530 3540
CAATTCACACTTTGGATTTATGATATATATGCACATGTAAGAGGGATGTATGCGCATAAT
GTTAAGGTTGAAACCTAAATACTATATATACGTGTACATTCTCCCTACATACGCGTATTA

3550 3560 3570 3580 3590 3600
TTATGATCTGAAATCAGAGACAGGCACGCGAAATGAATCGGAACACGGGATGTTATGCAT
AATACTAGACTTTAGTCTCTGTCCGTGCGCTTACTTAGCCTTGTGCCCTACAATACGTA

>dIns2_put._poly(A)_signal
|

3610 3620 3630 3640 3650 3660
GGTAGATATGTATGATTGTGCGGGGCCAGAATACATCGCCTGGGTATAAAATTATTAAATA
CCATCTATACATACTAACACGCCCCGGTCTTATGTAGCGGACCCATATTTAATAATTTAT

3670 3680 3690 3700 3710 3720
AATTATGTATTCAAACCTGCTGCAGATTGGCCAACTTGATTGGTAATGAAACGGGTATTAC
TTAATACATAAGTTTGACGACGCTTAACCGGTTGAACCTAACCATTAATTGCCCATAATG

<dIns4_put._poly(A)_signal
|

3730 3740 3750 3760 3770 3780
ATTGATTTTTCATTGTGCTTCATTGCAGTTAATTATTTATTGAACAGCGGCCGGATTTCT
TAACTAAAAAGTAACAGCAAGTAACGTCAATTAATAAATAACTTGTGCGCCGGCCTAAAGA

3790 3800 3810 3820 3830 3840
GTTTGCAACTATGTTGAAAAGGAAGCTGTGATTTTTTAACAAACTCTGTTTATTGTAAAG
CAAACGTTGATACAACTTTTCCTTCGACACTAAAAAATTGTTTGAGACAAGTAACATTTT

3850 3860 3870 3880 3890 3900
TTTAAATCATTCCAATTTAATGCCCTCAAAACCTACGCTGAAATGGTCAGTTTAAATAC
AAATTTTAGTAAGGTTAAATTACGGGAGTTTGGATGCGACTTACCAGTCAAAATTTTG

3910 3920 3930 3940 3950 3960
GATATTTATTAATATTTTAGTTAATTTACTAAGATTATCCGTTTTCGACTTTTAATGCCT
CTATAAATAATTATAAAATCAATTAAATGATTCTAATAGGCCAAAACGTGAAAATTACGGA

FIG. 4F

10/23

3970 3980 3990 4000 4010 4020
TGCATTTGGTAATGCGTGATTGTTATTTAAGGCTGTCATGAATTTAGTTGATTCCGTTTA
ACGTAAACCATTACGCACTAACAAATAAATTCCAGACGTACTTAAATCAACTAAGGCAAAT

4030 4040 4050 4060 4070 4080
TTTTAGCTTTCAAAATGTAATAATCTTCTAATTTACAACACACAGAACGATTAAATTAT
AAAATCGAAAGTTTTACATTATTAGAAGATTAAATGTTGATGTGTCTTGCTAATTTAATA

4090 4100 4110 4120 4130 4140
GAGTATTGCTATAAAATCGGCCAACCGCGACTAGAAATACTCGACTTTTAAGGTCAACAT
CTCATAACGATATTTTAGCCGGTTGGCGCTGATCTTTATGAGCTGAAAATTCCAGTTGTA

4150 4160 4170 4180 4190 4200
AAAAGTAAGTCAATGTTTTGATTATAAGATTTGATCAATTACTTCTTTACGGATGATATA
TTTTCAATTCAGTTACAAAATAATATTCTAAACTAGTTAATGAAGAAATGCCTACTATAT

4210 4220 4230 4240 4250 4260
ATCATCGATAAAACGAAGTACGAAAAAGCTATGAACTAAAATTTGGAAATTTCCCACATG
TAGTAGCTATTTGCTTCATGCTTTTTTCGATACTTGATTTTAAACCTTTAAAGGGTGAC

4270 4280 4290 4300 4310 4320
CGACTAACTTTTGAATTGCAATTGGATTGCTACTGTATTAAGACAGAAACAAGTTTTGG
GCTGATTGAAAACCTTAACGTTAACCTAACGGATGACATAATTTCTGTCTTTGTTCAAACC

4330 4340 4350 4360 4370 4380
AAATGAATGAATGGTTTAAATTGTTTCAAGTTTTTTTTAAGATTTTTTTTGTGTTTCAATAA
TTTACTTACTTACCAAATTTAACAAAGTTCAAAAAAATCTAAAAAAAACAAAAGTTATT

4390 4400 4410 4420 4430 4440
ATTTAGTTTTAATAGAAAAAAGATATATTCATTTTAGATTTCTGAATACTTGTGTTATA
TAAATCAAAATTATCTTTTTTCTATATAAGTAAATCTAAAGACTTATGAACACAATAT

4450 4460 4470 4480 4490 4500
TCGCTTTTTATTCAAGTGTAATAATCAACATATATATCATATAATGATAATAATAAATGT
AGCGAAAAATAAGTTCACATTATTAGTTGTATATATAGTATATTACTATTATTATTACA

4510 4520 4530 4540 4550 4560
AACGTCCCAAATTAATAATAATATAAAGTAGCATTTGCGATTGTTTGCCAAAGCTTAAAG
TTGCAGGGTTTAATTATTATTATATTTTCATCGTAAACGCTAACAAACGGTTTCGAATTTT

4570 4580 4590 4600 4610 4620
CAGAATATATATTTAATCCATTTTCGATCATTCGTAAAGAGTAACATGCAACAAGCTGTAA
GTCTTATATATAAATTAGGTAAAGCTAGTAAGCATTTCTCATTTGTACGTTGTTTCGACATT

4630 4640 4650 4660 4670 4680
AAAACATCGATTGTAGTATATATGCACATGGTTGGTTTGGAAACCAGATTCAGAGATAATC
TTTTGTAGCTAACATCATATATACGTGTACCAACCAAACCTTGGTCTAGGTCTCTATTAG

4690 4700 4710 4720 4730 4740
GCGTCGACCAGGTCAAGTTGGGGTCAATGATTTTCGCATTAGGAGGCCTAATTTCTGACCA
CGCAGCTGGTCCAGTCAACCCAGTTACTAAAAGCGTAATCCTCCGGATTAAAGACTGGT

< * N R V V
< _____

FIG. 4G

11/23

4750 4760 4770 4780 4790 4800
 CGGAGCAGTACTCCCGCAGAGCCTTCATATCACAGGACTTTTTCGAGCACCTCTCCACGA
 GCCTCGTCATGAGGGCGTCTCGGAAGTATAGTGTCTGAAAAACGTCGTGGAGAGGTGCT
 <S C Y E R L A K M D C S K K C C R E V I
 <_____DINS4 CODING REGION (EXON-2)_____

4810 4820 4830 4840 4850 4860
 TTCCTTGCCGTTGGCGAGTTCGCCTCCGGACTTCAGCCAGGGAATTGAGTACACCCCCAA
 AAGGAACGGCAACCGCTCAAGCGGAGGCCTGAAGTCGGTCCCTTAACTCATGTGGGGGTT
 <G Q R Q R T R R R V E A L S N L V G G L
 <_____DINS4 CODING REGION (EXON-2)_____

4870 4880 4890 4900 4910 4920
 GATAGCTCCCAGGAAAGAGGGCACTTCGCAGCGGTTCCGATATCGAGTTATCCTCCTCCT
 CTATCGAGGGTCTTTCTCCCGTGAAGCGTCGCCAAGGCTATAGCTCAATAGGAGGAGGA
 <Y S G P F L A S R L P E S I S N D E E E
 <_____DINS4 CODING REGION (EXON-2)_____

4930 4940 4950 4960 4970 4980
 CGAACTCCTGGACAAACTGCAGGGGATTGAGGGCGTCCAGATCGCTGTGGGCACCGGCTA
 GCTTGAGGACCTGTTTGACGTCCCTAACTCCCGCAGGTCTAGCGACAGCCGTGGCCGAT
 <F E Q V F Q L P N L A D L D S D A G P
 <_____DINS4 CODING REGION (EXON-2)_____

4990 5000 5010 5020 5030 5040
 ATAAAAATCGTGATACAATGTAGATCTAGCAAAGCCAGCTTGAGGATCTGCATCCTTGT
 TATTTTTAGCACCTATGTTACATCTAGATCGTTTCGGTCGAACTCCTAGACGTAGGAACA

5050 5060 5070 5080 5090 5100
 AAGAACTTACGCATGGCGCGCTTGTGTGGAATCACGGGATTATACTCCTCGCACACCATA
 TTCTTGAATGCGTACCGCGCGAACACACCTTAGTGCCCTAATATGAGGAGCGTGTGGTAT
 <M A R K H P I V P N Y E E C V M
 <_____DINS4 CODING REGION (EXON 1)_____

5110 5120 5130 5140 5150 5160
 CTCAGCACCTCGTTGAGCTTTTCACTGCAGAGCGTTCCTTGGGCCAACTTCACTGTGGAG
 GAGTCGTGGAGCAACTCGAAAAGTGACGTCTCGCAAGGAACCCGGTTGAAGTGACACCTC
 <S L V E N L K E S C L T G Q A L K V T S
 <_____DINS4 CODING REGION (EXON 1)_____

5170 5180 5190 5200 5210 5220
 CTGGCCAGCAAAATCACGGCCACCATCGAGATGAAGGACAAAGGCTTGCTCATGGTTATG
 GACCGGTGCTTTTAGTGCCGGTGGTAGCTCTACTTCCGTGTTTCCGAACGAGTACCAATAC
 <S A L L I V A V M S I F S L P K S M
 <_____DINS4 CODING REGION (EXON 1)_____

5230 5240 5250 5260 5270 5280
 GGTTTACTGCTTAGGTTGCTTTACGATCAAATGGATTAAAGTTGGGTGAGCCGGGTGCGAA
 CCAAATGACGAATCCAACGAAATGCTAGTTTACCTAATTCAACCCAGCTCGGCCAGCTT

FIG. 4H

12/23

5290 5300 5310 5320 5330 5340
AGCTAACTGATGATGTTTGGCCCAAAGTAACTGGCTTATATACTGCCTCGTAAGAACTT
TCGATTGACTACTACAAACCGGGTTTCATTGACCGAATATATGACGGAGCATTCTTTGAA
<_____DINS4 PUT. PROMOTER_____>

5350 5360 5370 5380 5390 5400
AAACTGGGTCTGGGTCTGGGTCTGGGTCTGGGTCTGGGTCTGGATCCACACACATGTT
TTTGACCCAGACCCAGCCCCAGCCAGAGAGCCCCAGCCCCAGACCTAGGTGTGTGTACAA

5410 5420 5430 5440 5450 5460
ATCCTCAAAAGTCAGGTGTCAAATTGTGTTAGGATGCGATGAGTGCATTCCGGAGTTGG
TAGGAGTTTTTCAGTCCAACAGTTTAAACACAATCCTACGCTACTCACGTAAGGCCTCAACC

5470 5480 5490 5500 5510 5520
CTCTTCTCTCTAAACGCTGGCTAAACTCATTCAATGTCAAAGCTGACTTATGCAAATGGC
GAGAAGAGAGATTGCGGACCGATTGAGTAAGTTACAGTTTCGACTGAATACGTTTACCG

5530 5540 5550 5560 5570 5580
TATTGGAAAATTGTGGGTGGTTTTTGGGTGGCTGTGTTTTGGGAGAAGAAGGGCTTTGTGG
ATAACCTTTTAACACCCACCAAAAACCCACCGACACAAACCTCTTCTTCCCGAAACACC

5590 5600 5610 5620 5630 5640
GCGTTTTGCTGTCAGCCAATTAAACAATTTATGTATAAACAGCCAGGCCGTACTAAGCCC
CGCAAAACGACAGTCGGTTAATTTGTTAAATACATATTTGTCTGGTCCGGCATGATTCCGG

5650 5660 5670 5680 5690 5700
TGCATTTATGAATACCAAATAAGTCCTTGGTCTTAAAGTTACCTCGCCTTTACAGCCCGT
ACGTAAATACTTATGGTTTATTCAGGAACCAGAATTTCAATGGAGCGGAAATGTCTGGGCA

5710 5720 5730 5740 5750 5760
TTGCCTCTACCATTTCTACCCCTATACTTACCAATCCGCGCCTGGGCGCCCGGCAGGCCGG
AACGGAGATGGTAAAGATGGGATATGAATGGTTAGGCGCGGACCCGCGGGCCGTCCGGCC

5770 5780 5790 5800 5810 5820
AGTAGGCCAACAAGAACCCGAGCCAGCTGATTGGAGCCAGCAGCATCCTGGCAACGAATT
TCATCCGGTTGTTCTTGGGCTCGGTCTGACTAACCTCGGTCTGCTAGGACCGTTGCTTAA

5830 5840 5850 5860 5870 5880
ACGCCTCCTTGGTACTTTTCTTTGACTGTCTTGTCTTTGCGGCTCACACAAATTCCTTCT
TGCGGAGGAACCATGAAAAGGAACTGACAGAAACAGAAACGGCGAGTGTGTTTAAAGAAGA

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|

5890 5900 5910 5920 5930 5940
TTTTGCACTGTCTACTTTTATTCATTAGTCAAAGTTGGTGTCTGCATAAATAAGTGATTAC
AAAACGTGACAGATGAAAATAAGTAATCAGTTTCAACCACGACGTATTTATTCACTAATG

5950 5960 5970 5980 5990 6000
GAATTGGATTACGAATGCTGTTAGGAGAACGGGTGTACATATAGTATGTATGTGGGAATG
CTTAACCTAATGCTTACGACAATCCTCTTGCCACATGTATATCATACATACACCCCTTAC

FIG. 4I

6010 6020 6030 6040 6050 6060
CCATGTTCAAGTGTTCGTATGTATGTATGTATGTATGTCATGCTGGGTAATGAATGTGT
GGTACAAGTTCACAAGCATACATACATACATACATACGTACGACCCATTACTTACACA

6070 6080 6090 6100 6110 6120
GTGTGTTGGCCAAGTGTCTATTTCGGTAGACAGTAGATGGCTAACTCCAAGTAGCTGCA
CACACAACCGGTTACAGGATAAAGCCATCTGTCTATCTACCGATTGAGGTTTCATCGACGT
<* K P L C Y I A L E L Y S C
<_____DINS3 CODING REGION_____

6130 6140 6150 6160 6170 6180
GGTCTTGACGCAGCACTCGTCTAGACGCCACCGGTCAGGTGTCTCTGTGGCGACGCAT
CCAGAACTGCGTCTGTGAGCAGCATCTGCGGTGGCCAGTCCACAGAGGACACCGCTGCGTA
<T K V C C E D Y V G G T L H R R H R R M
<_____DINS3 CODING REGION_____

6190 6200 6210 6220 6230 6240
CTTGATCAGGACCTCGGATCCGTACAGATTGGTTAGCAGTGGACTAAAAGAGTATCCTGC
GAACTAGTCTCGGAGCCTAGGCATGTCTAACCAATCGTCACCTGATTTTCTCATAGGACG
<K I L V E S G Y L N T L L P S F S Y G A
<_____DINS3 CODING REGION_____

6250 6260 6270 6280 6290 6300
CCCGTCCAGTGTCTGCCACATGCTGCTATCATCCTGCACCTCCTGCTCCGTGTCTCTCGTC
GGGAGGTACAGACGGTGTACGACGATAGTAGGACGTGGAGGACGAGGCACAGGAGCAG
<G D L T Q W M S S D D Q V E Q E T D E D
<_____DINS3 CODING REGION_____

6310 6320 6330 6340 6350 6360
GTCGTCGCTGTTGCCAGCAAGCTTTACGTTTCCTTGGCAGCGTATTAAAGCCATGGGG
CAGCAGCGACAACGGGTGCTTCGAAAGTGCAAAGGAACCGTCCGATAATTTGGGTACCCC
<D D S N G L L S E R K R P L T N F G H P
<_____DINS3 CODING REGION_____

6370 6380 6390 6400 6410 6420
ACACACCACATCCATGGCATCGGACAGTGCAGGGCCGAGAGTTTGTGGTTTCCGGGGGG
TGTGTGGTGTAGGTACCGTAGCCTGTACGCCCCGGCGTCTCAAACACCAAAGGCCCCCC
<C V V D M A D S L A P G C L K H N G P P
<_____DINS3 CODING REGION_____

6430 6440 6450 6460 6470 6480
CAGCAACTGGTGACCACTGCCAGTCGGCGTGACCATTGCCATTGCAGCGGTGAGCATGGC
GTCGTTGACCACTGGTGACGGTCAGCCGCACTGGTAACGGTAACGTCCGCACTCGTACCG
<L L Q H G S G T P T V M A M A A T L M A
<_____DINS3 CODING REGION_____

6490 6500 6510 6520 6530 6540
TGCGATGAGCAGCGACTGGAGCCGAAGGCCATGTACTGCTGCACCGTTGTGCTGGCTAAA
ACGCTACTCGTCTGACCTCGGCTTCCGGTACATGACGACGTGGCAACACGACCGATTT
<A I L L S Q L R L G H V A A G N H Q S F
<_____DINS3 CODING REGION_____

FIG. 4J

14/23

6550 6560 6570 6580 6590 6600
CATCTTGGATATGCAGTGAATGCTCTGGGCTGCAACTGGTATTTATACCCTAAATCGGA
GTAGAACCCTATACGTCACTTACGAGACCCGACGTTGACCATAAAATATGGTGATTTAGCCT
<M
<_____

6610 6620 6630 6640 6650 6660
AGCGCTAGCTAATGCAGTTCAATGGCCTCTTCTGCAGTCTAGCATTGCAGTGGCATAGCA
TCGCGATCGATTACGTCAAGTTACCGGAGAAGACGTCAGATCGTAACGTCACCGTATCGT
<_____DINS3 PUT. PROMOTER_____

6670 6680 6690 6700 6710 6720
AGCCCCACGGGCGTACAAACTGCAAATCCTTTGATCACCCATGTTTCAGGTACCGTTTTT
TCGGGGTGCCCGCATGTTTGACGTTTAGGAACTAGTGGGTACAAAGTCCATGGCAAAA

6730 6740 6750 6760 6770 6780
CCCCTAAAAATGCAAACTCTATTTCTAGCTCTACTCCCCAATTTGGATGGAAAAGCGATG
GGGATTTTTTACGTTTGAGATAAAGATCGAGATGAGGGGTAAACCTACCTTTTCGCTAC

6790 6800 6810 6820 6830 6840
CACTGTTGTTTTGGTAGTTGGGGTATTGTATTGTATTTCTTAGCAAATATCAGTTGTATC
GTGACAACAAAACCATCAACCCATAACATAAAGAATCGTTTATAGTCAACATAG

6850 6860 6870 6880 6890 6900
ATTACCTATATCTATCTATACCAATAGTTTGGAAATGTATTTGTAAGACATTTTAAAGATA
TAATGGATATAGATAGATATGGTTATCAAACCTACATAAAACATTCTGTAAAAATTCTAT

6910 6920 6930 6940 6950 6960
TTCAGAAGAGTTAGCCTTATGGGACTTGCTCTAAAGTGTGAATTGATGCACACAGCTTTA
AAGTCTTCTCAATCGGAATACCCTGAACGAGATTTACACTTAACTACGTGTGTGAAAT

6970 6980 6990 7000 7010 7020
TCGAGCATAGTTTTCAGTGTAATCACCGCCAAAAAATCCGCCCCTTCAAAGCATAACCC
AGCTCGTATCAAAAGTCACATTAGTGGCGGTTTTTTAGGCGGGTGAAGTTTCGTATTGGG

7030 7040 7050 7060 7070 7080
GTTCCGCCAACCTGTTACATTGCCGCTAAGAGGCTCTGACTGCTGTGCGATTGCGATTACG
CAAGCGGGTTGGACAATGTAAACGGCGATTCTCCGAGACTGACGACAGCTAACGCTAATGC

7090 7100 7110 7120 7130 7140
ATTACGACCAGATATCTGTGGGGCATGGGGATAAGGGGTATGTGGGCGGATGGCTGACAG
TAATGCTGGTCTATAGACACCCCGTACCCCTATTCCCCATACACCCGGCTACCGACTGTC

7150 7160 7170 7180 7190 7200
TGTGGCAGCCTCATTAGCATGTGCTGGCCAGGAGGAAAGTATGCTTCGATGAAGCTCCTC
ACACCGTTCGGAGTAATCGTACAGCACCGGTCTCTTTTCATACGAAGCTACTTCGAGGAG

7210 7220 7230 7240 7250 7260
CGGCGGCAGTGTGCGAAATCGCTTCGATCACCATCATCGCCATCGCCATGGCCACTCGAT
GCCGCCGTCAACGCTTTAGCGAAGCTAGTGGTAGTAGCGGTAGCGGTACCGGTGAGCTA

FIG. 4K

7270 7280 7290 7300 7310 7320
TGTCGAGTTGCACGCACGGCGATGCCAACAGTTGGTTGCCAGCGCTGCACTCGAAACACT
ACAGCTCAACGTGCGTGCCGCTACGGTTGTCAACCAACGGTCGCGACGTGAGCTTTGTGA

7330 7340 7350 7360 7370 7380
CGCTTCTTCCCACCGACCGCAAAGTGCCGGAAGCTAGAAAAAAGCAAAAAAAGT
GCGAAGAAGGGTGGCTGGCGTTTACGGCCTTTTCGATCTTTTTTTCGTTTTTTTTTCA

7390 7400 7410 7420 7430 7440
GGAAGAAAATTCGCGATAGAAAACGGAAAAATCGAAACGAACAAAAAAGTCGGAATAAA
CCTTCTTTTAAGCGCTATCTTTTGCCTTTTTAGCTTTGCTTGTTTTTTTCAGCCTTATTT

7450 7460 7470 7480 7490 7500
TCAAGGAAACATGGTGTCTCGACATTAAGATGTGCCGATTTGATAATGTGCCCTGGGGCTT
AGTTCCTTTGTACCACGAGCTGTAATTCTACACGGCTAAACTATTACACGGGACCCCGAA

7510 7520 7530 7540 7550 7560
TCGCCTGGTGGGCGGGGCGGACTACGATTATCCGCTGACGGTGGTTAAGGTTAGGCCCGA
AGCGGACCACCCGCCCGCCTGATGCTAATAGGCGACTGCCACCAATTCCAATCCGGGCT

7570 7580 7590 7600 7610 7620
TTCGAAAAAAGAACGAAATCTATATGCTGCAACCCCCACCCCCCACGCATCACCTCAGC
AAGCTTTTTTCTTGCTTTAGATATACGACGTTGGGGGTGGGGGGGTGCGTAGTGGAGTCG

7630 7640 7650 7660 7670 7680
CCATTCACCTGGCGGATGTTTCATAGACCAGTGGAAAAATATTGCTCACTATGCAGCTGATG
GGTAAGTGGACCGCCTACAAGTATCTGGTCACCTTTTATAACGAGTGATACGTCGACTAC

7690 7700 7710 7720 7730 7740
AATCACATTGGATTAATTTCGATACGATACGTTTGAATCAGTTTTATTTGTTTCGATTGCAA
TTAGTGTAACTAATTAAGCTATGCTATGCAAGCTTAGTCAAAATAAACAAAGCTAACGTT

7750 7760 7770 7780 7790 7800
TATTACGTAACGCCGCGATGCGTGTGTGTCCATTTCGGATTTGCTGCATTGGCAAATTAGT
ATAATGCATTGCGGCGCTACGCACACACAGGTAAGCCTAAACGACGTAACCGTTTAATCA

7810 7820 7830 7840 7850 7860
TAATTAAGTAATTCTCTCGCTTTTGTTTTATCTAATCGACAGGGCCATACATTTCCCGC
ATTAATTTTCATTAAGGAGAGCGAAAACAAATAGATTAGCTGTCCCGGTATGTAAAGGGCG

7870 7880 7890 7900 7910 7920
TAATGAGCCGCATAATGGCAGCGGCAATAAACTTATTCAAATTTTAATTGTGTTTCGCTG
ATTACTCGGCGTATTACCGTCGCGTTATTTGAATAAGTTTAAATTAACACAAAGCGAC

7930 7940 7950 7960 7970 7980
GCAGTTGGTCCTTTGTTTGTGTCATAAATTGCATTTGGCAATTTCGCATTTTGTAAACATTGT
CGTCAACCAGGAAACAAACACGTATTTAACGTAAACCGTTAAGCGTAAACACATTGTAAAC

7990 8000 8010 8020 8030 8040
GTTGACAAATTCGCAACCAGCAACAATAACAAAAATACAATACATACTATAGCATC
CAACTGTTAAGCGTTGGTCGTTGTTATTTGTTTTATGTTATGTATGTTATGATATCGTAG

FIG. 4L

16/23

8050 8060 8070 8080 8090 8100
GTCGTAAATCCGAAACAAATGCGATTTTTTAATTGGCAAACCTGCTAAGCGCATAAACAAA
CAGCATTTAGGCTTTGTTTACGCTAAAAATTAACCGTTTGACGATTGCGGTATTTTGTTT

8110 8120 8130 8140 8150 8160
TGACCGAAATGCGAGGGGCGCTAAAAATCCCATCCCTTCGATACGAATAAATCAATTTA
ACTGGCTTTACGCTCCCCGCGATTTTTTAGGGTAGGGAAGCTATGCTTATTTAGTTAAAT

8170 8180 8190 8200 8210 8220
AGCCGCAGAGTCAAGGAAGGGAGGTCATAAATTGTTTTTGACTTTTTGGTTATTTTTTTT
TCGGCGTCTCAGTTCCCTCCCTCCAGTATTTAACAAAACTGAAAAACCAATAAAAAAA

8230 8240 8250 8260 8270 8280
TTACCGTTTTACATAAACAAATTATGCTATGGGTATTTTTTAAATTCCGATCAATTTATAA
AATGGCAAAATGTATTTGTTTAATACGATACCCAATAAAATTTAAGGCTAGTTAAATATT

8290 8300 8310 8320 8330 8340
AATGTTTGTGCTTTGGGATATGCATACCATGAAAAAATGGAAGTTTATTGTAAATGAATT
TTACAAACACGAAACCCCTATACGTATGGTACTTTTTTACCTTCAAATAACATTTACTTAA

8350 8360 8370 8380 8390 8400
ATTAACCTTCACAAGCTGGCTGATAGAGAAAAAAGCTGAAAAATGTCCGGAATGTTCTTCAT
TAATTGAAGTGTTGACCGACTATCTCTTTTTTGACTTTTTTACAGGCCTTACAAGAAGTA

8410 8420 8430 8440 8450 8460
TCCAATGAACTCCCTAAATTAACTTAGCTAATTTATTCCTTATACTAATACTCCGCTTTT
AGGTTACTTGAGGGATTTAATTGAATCGATTAAATAAGGAATATGATTATGAGGCGAAAA

8470 8480 8490 8500 8510 8520
AAGAATTCCTTACTACATGTTAGAGACTCAAAAAGCACATCCTTCGACTCGAGTCCATAT
TTCTTAAGGAATGATGTACAATCTCTGAGTTTTTCGTGTAGGAAGCTGAGCTCAGGTATA

8530 8540 8550 8560 8570 8580
TACTTTATGGAATGTGCCAACACACCTTCACATATTGGCTCTGCAACACTAAACAATCC
ATGAAATACCTTACACGGTTGTGTGGAAGTGTATAACCGAGACGTTTGTGATTTGTTAGG

8590 8600 8610 8620 8630 8640
TTGGTAATCTTTTGAAAAACCTCTGTTTACACTACCACTCTTCGTCATGCTGCTCGCCAC
AACCATTAGAAAACTTTTTGAGAGACAAATGTGATGGTGAGAAGCAGTACGACGAGCGGTG

8650 8660 8670 8680 8690 8700
ATACAGTCTGGTACATAGATGTATGGCCCAGCTAAGCCCAAAGCCTTTGTTCTATAAATA
TATGTCAGACCATGTATCTACATACCGGTCGATTTCGGGTTTCGGAAACAAGATATTTAT

8710 8720 8730 8740 8750 8760
TTCGCAACCTCCGACGATGTCGAGTGCTTTTTTGCTCTGCGAATTCACCGCTGGAAATTGA
AAGCGTTGGAGGCTGCTACAGCTCACGAAAAACGAGACGCTTAAGTGGCGAGCTTTAACT

8770 8780 8790 8800 8810 8820
CTCTACCATAAGTGAAATGCAAGAGACCCCTGGGACTGAAAGGAAAGACCCCTCAACTTGG
GAGATGGTATTCACTTTACGTTCTCTGGGGACCCCTGACTTTCCTTTCTGGGAGTTGAACC

FIG. 4M

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8830 8840 8850 8860 8870 8880
TTGGGTGAAATGGTGGAGTCTCCAACCTCCACCTGCTCCTTGTGCCAACCACTTTTTTTT
AACCACCTTTACCACCTCAGAGGTTGGGAGGTGGACGAGGAACACGGTTGGTGAAAAAAA

8890 8900 8910 8920 8930 8940
TTTTTGCAGTATTTGCATTACTAAGTCTCTTGGCAGTCGGTGTCTGTGACTTTCTGGTTA
AAAAACGTCATAAACGTAATGATTTCAGGAGAACCCTCAGCCACAGCACTGAAAAGACCAAT

8950 8960 8970 8980 8990 9000
TGAACCTGCTTTCTCATAACGGAAACGAAAAACAATCGCGTTTATTTGCCCACGAAAGTG
ACTTGGGACGAAAGAGTATTGCCTTTGCTTTTGTTAGCGCAAATAAACGGGTGCTTTTCAC

9010 9020 9030 9040 9050 9060
TTACAAAACCTGCCTGAATTATGCAATAGAATTCTTTGAACAGAGTGCTAAGATATTTTCGC
AATGTTTTGACGGACTTAATACGTTATCTTAAGAACTTGTCTCACGATTCTATAAAGCG

9070 9080 9090 9100 9110 9120
ATTTTGAAGGCGAAACATAATTCATCCATAACTATTAGTTTGATGAATTCTCACTTCGTA
TAAACTTCCGCTTTGTATTAAAGTAGGTATTGATAATCAAATACTTAAGAGTGAAGCAT

9130 9140 9150 9160 9170 9180
TGCTGGCAATTTTGAAGGCCGAAGTGGCAAAACCATTTTAAATGAATTCCTACAATTTAT
ACGACCGTTAAACTTCCGGCTTCACCGTTTGGTAAAATTTACTTAAGGATGTTAAATA

9190 9200 9210 9220 9230 9240
ATGCTCAATTTGCGCCAATTTGTCTGTACTTTATTACCCACAAAAGCCATAAAGCTTATA
TACGAGTTAAACGCGGTTAAACAGACATGAAATAATGGGTGTTTTTCGGTATTTTCGAATAT

9250 9260 9270 9280 9290 9300
TTGTATTTAGTTGTTATTTGTTCTCGCAACATTTTCACTTTGATTTATAGTTGCGAAAATA
AACATAAATCAACAATAACAAGAGCGTTGTAAAAGTGAACTAAATATCAACGCTTTTAT

9310 9320 9330 9340 9350 9360
AATGTTGGCAAATGCAAATTTTGAACGATATTCTCTTACACGGTCATTTGGTACCATT
TTACAACCGTTTACGTTTAAAACTTTGCTATAAGAGAATGTGCCAGTAAACCATGGTAA

9370 9380 9390 9400 9410 9420
TCCGGAATATACATTTACCAATTTTCCAAAAAAGAGCCATAAATTGTATTATCCAATTA
AGGCCTTATATGTAAATGGTTAAAAGGTTTTTTTCTCGGTATTTAACATAATAGGTTAAT

9430 9440 9450 9460 9470 9480
AAACGATTAGTCCAGTGGGTTTTTATTTCTAAAAATTTAATTTTGTAAATTAGAGAAAACCT
TTTGCTAATCAGGTCACCCAAAAATAAAGATTTTAAATTAAACATTAATCTCTTTTGA

9490 9500 9510 9520 9530 9540
ATTGTGAACCTTTGGATGACCTAGAAAGTTTCATTAGTTGTACATTATTTTACCCCCGC
TAACACTTGAAACCTACTGGATCTTCAAAGTAATCAACATGTAATAAAAAATGGGGGCG

9550 9560 9570 9580 9590 9600
TTTAAATTTGCAGAACTTCTGTAAAAAAGCTTTTACAAGCTATTTAAATATTAGTGGT
AAATTTTAAACGTCTTGAAGACATTTTTTTTCGAAAATGTTTCGATAAATTTATAATCACCA

FIG. 4N

9610 9620 9630 9640 9650 9660
AGAGTTGTTTGAACATTTATCTTTTTTGGAAATCAGCAATATTTGGTTCTCTATCCTTACAA
TCTCAACAAACTTGTAAATAGAAAAACCTTAGTCGTTATAAACCAAGAGATAGGAATGTT

9670 9680 9690 9700 9710 9720
ATTAATCTTCTCTTTAAGTGAACCTCATAACTTTGTATATATGTACGTATGTAGAATCATC
TAATTAGAAGAGAAATTCACCTTGAGTATTGAAACATATATACATGCATACATCTTAGTAG

9730 9740 9750 9760 9770 9780
CTTCAACTCAAACATTTCCATCCGGCGAAACAATGCAATATTTGAGTGGTTAGACATGGG
GAAGTTGAGTTTGTAAGGTAGGCCGCTTTGTACGTTATAAACTCACCAATCTGTACCC

9790 9800 9810 9820 9830 9840
TAATTCACCTTGACTCGCTTAACTGAAGTGTCGTTAATGAGCTGCCACTTCTACTCGAGC
ATTAAGGTGAACTGAGCGAATTGACTTCACAGCAATTACTCGACGGTGAAGATGAGCTCG

9850 9860 9870 9880 9890 9900
ACCCCTCGTTCTGAGCCCCCAGCCCCACAGATCCTCTGTAGCCCCCCCATCTCCTTGGG
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9910 9920 9930 9940 9950 9960
CATTGTCTTCGGTTCTGTTGGGTTTGTGCGTGATTGTATGATTGTCTGTTCTGGGGGTCTG
GTAACAGAAGCCAAGACAACCCAAACACGCACTAACATACTAACAGACAAGCCCCCAGAC

9970 9980 9990 10000 10010 10020
GGTCTGCTGGTCTTTGTTTTGTTGACATTTGGCGCGCGTTTTATTTTTATGCACTTAGCA
CCAGACGACCAGAAACAAACAACCTGTAAACCGCGCGCAAATAAAAATACGTGAATCGT

10030 10040 10050 10060 10070 10080
CGCGACGTCGCGCTGTGCGCTAATAGAAATTTCCCCATTATCGCATCGCATCCCATTGT
GCGCTGCAGCGGCAACAGCCGATTATCTTTAAAGGGTAATAGCGTAGCGTAGGGTAACA

10090 10100 10110 10120 10130 10140
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TAACATAGAGCCGATAGAGCTGATAGAGCCGGAGCGTGAGTAAGATAGCGGTGTAAGGGT

10150 10160 10170 10180 10190 10200
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10210 10220 10230 10240 10250 10260
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10270 10280 10290 10300 10310 10320
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10330 10340 10350 10360 10370 10380
GCCTCATTATGGGCAGTGGAAGCGTCTTCTATTTTGGCGTCTACCGGTGAGCTTTCCCAT
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FIG. 40

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10390 10400 10410 10420 10430 10440
CCTTCTATTCCATACCATTCCTGTTTCGTCTCTTACTGCTCGTGGTGGTGGTCCCTCGTCC
GGAAGATAAGGTATGGTAAGGCAAAGCAAGAGAATGACGAGCACCAGCACCAGGAGCAGG

10450 10460 10470 10480 10490 10500
TTGTCCGGTTCCCTTTACTACTACTCTTTGTATCCCATCCACCGAGGACCATTATCACAG
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10510 10520 10530 10540 10550 10560
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10570 10580 10590 10600 10610 10620
TTCAAGAAATTACAAAACCAACAAACGACCTCGAGAGAAATGGAAAAAATATGACAAATTT
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10630 10640 10650 10660 10670 10680
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10690 10700 10710 10720 10730 10740
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10810 10820 10830 10840 10850 10860
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11050 11060 11070 11080 11090 11100
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AGTGGTTACGGCTGGTAAAGTGGCAGCGGCTGAGGTAGCGACAGGGTCGACTGCCTTTGG

11110 11120
ACAAATGCCCGTACTCCGGA
TGTTTACGGGCATGAGGCCT

FIG. 4P

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10 20 30 40 50 60
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K G I E K R C Q>
CODING REGION
K G I E K R C Q>
SIGNAL PEPTIDE

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D R R I L L P S L L L L I L H I G G V Q>
CODING REGION
D R R I L L P S L L L L I L H I G G V Q>
SIGNAL PEPTIDE

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A T H K L C G R K L P E T L S K L C V Y>
CODING REGION
A>
T H K L C G R K L P E T L S K L C V Y>
B PEPTIDE

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G F H A K T K R T L D P V H F H Q I D G>
CODING REGION
G F H A K T>
B PEPTIDE
K R T L D P V H F H Q I D G>
C PEPTIDE

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F E D R S L L E R L L S D S S V Q K L K>
CODING REGION
F E D R S L L E R L L S D S S V Q K L K>
C PEPTIDE

310 320 330 340 350 360
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CODING REGION
T R R>
L R D G V F D E C C L K S C T H D>
A PEPTIDE

370 380 390 400 410 420
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E V L R Y C A A K P R T>
CODING REGION
E V L R Y C A A K P R T>
A PEPTIDE

AATG
TTAC

FIG. 5

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 ACTGCAATAGCTAGGCTTTCGATTTAGTGTGATATAAATACAGTTGCAAGGCAAGGCAAT
 TGAAGTAATGATGAGGCAAGGCTAAATCAACATATTTATGGTCAAGGCTGCTGTGTA

70 80 90 100 110 120
 CACTGCAATAGCTAGGCTTTCGATTTAGTGTGATATAAATACAGTTGCAAGGCAAGGCAAT
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 K F S Q R H G A A V H G L R L>
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 SIGNAL PEPTIDE

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 CODING REGION
 Q S L L I A A K L T A A K A>
 SIGNAL PEPTIDE
 K V T P T G>
 B PEPTIDE

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 CODING REGION
 S G H Q L L P F G H H K L C G P A L S D>
 B PEPTIDE

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 A K D V V C F H G F H T L P>
 B PEPTIDE
 R K R E S L>
 C PEPTIDE

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 CODING REGION
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 C PEPTIDE

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 CODING REGION
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 S E V L I K H R R R H R R H L T G G V Y D>
 CODING REGION
 S E V L I K H R R R H R R>
 C PEPTIDE
 R L T G G V Y D>
 A PEPTIDE

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 E C C V K T C S Y L E L A I Y C L P K>
 CODING REGION
 E C C V K T C S Y L E L A I Y C L P K>
 A PEPTIDE

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 AAGGCAAGGCTGCTCATGAGGCAAGGCTGCTCATGAGGCAAGGCTGCTCATGAGGCAAGGCTGCT
 AAGGCAAGGCTGCTCATGAGGCAAGGCTGCTCATGAGGCAAGGCTGCTCATGAGGCAAGGCTGCT
 TOCTTGTGA

FIG. 6

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K S K P L S F I S H V A V I L L A S S T>
      CODING REGION
K S K P L S F I S H V A V I L L A S S T>
      SIGNAL PEPTIDE

      70      80      90      100     110     120
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CACTTCAGAGGCTTCTGCGAGAGCTCACTTTTGGAGTTGCTCCAGAGCTCATACAC
V K L A Q G T L C S E K L H E V L S K V>
      CODING REGION
V K L A Q G>
      SIGNAL PEPT
      T L C S E K L H E V L S K V>
      B PEPTIDE

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C E E Y N P V I P H K R A K P G A D S D>
      CODING REGION
C E E Y N P V I P H>
      B PEPTIDE
      K R A K P G A D S D>
      C PEPTIDE

      190     200     210     220     230     240
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GAGCTAAGGAGGAGTTAGGCGAGGTCAGAGAGGCTGCTCAAGCTGCTGCTGCTATTGAGCTAT
L D A L N P L Q F V Q E F E E E D H S I>
      CODING REGION
L D A L N P L Q F V Q E F E E E D H S I>
      C PEPTIDE

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AGGCTTGGGAGGCTTCAAGGCGAGAGGAGGAGGCTGATAGAGGCGGAGATGAGTTAAGG
S E P L R S A L F P G S Y L G G V L H S>
      CODING REGION
S E P L R S A L F P G S Y L G G V L H S>
      C PEPTIDE

      310     320     330     340     350     360
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L A E V R R R T R Q R Q G I V E R C C K>
      CODING REGION
L A E V R R R>
      C PEPTIDE
      T R Q R Q G I V E R C C K>
      A PEPTIDE

      370     380     390     400     410     420
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      CODING REGION
K S C D K K A L R E Y C S V V R H>
      A PEPTIDE

      430     440
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FIG. 7

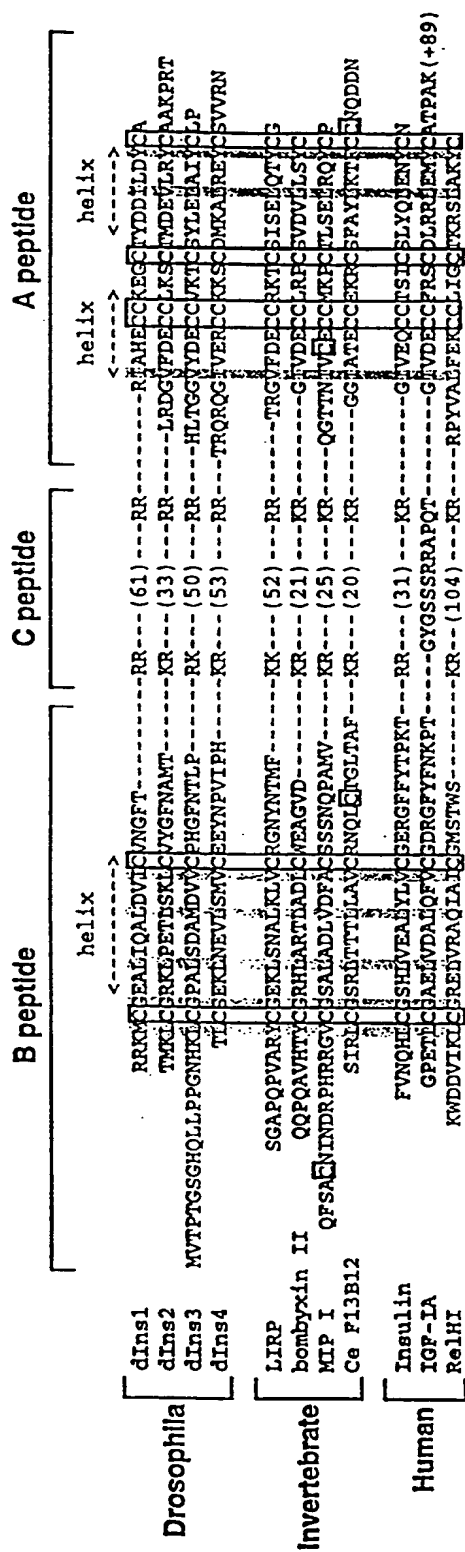


FIG. 8

SEQUENCE LISTING

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INSULIN-LIKE GENES AND USES THEREOF

<130> 7326-066-228

<140>

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<150> 09/201,227

<151> 1998-11-30

<160> 15

<170> PatentIn Ver. 2.0

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<213> Drosophila melanogaster

<400> 1

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Leu Cys Gly Arg Lys Leu Pro Glu Thr Leu Ser Lys Leu Cys Val Tyr
      35             40             45

Gly Phe Asn Ala Met Thr Lys Arg Thr Leu Asp Pro Val Asn Phe Asn
      50             55             60

Gln Ile Asp Gly Phe Glu Asp Arg Ser Leu Leu Glu Arg Leu Leu Ser
      65             70             75             80

Asp Ser Ser Val Gln Met Leu Lys Thr Arg Arg Leu Arg Asp Gly Val
      85             90             95

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<213> Drosophila melanogaster

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Cys Gly Pro Ala Leu Ser Asp Ala Met Asp Val Val Cys Pro His Gly
      50           55           60

Phe Asn Thr Leu Pro Arg Lys Arg Glu Ser Leu Leu Gly Asn Ser Asp
      65           70           75           80

Asp Asp Glu Asp Thr Glu Gln Glu Val Gln Asp Asp Ser Ser Met Trp
      85           90           95

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50 55 60
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85 90 95
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130 135

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<211> 11120
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<400> 7

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/28315

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) :C07H 21/04; C07K 14/00; C12N 15/85

US CL :435/325; 530/350; 536/23.1; 536/23.5

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/325; 530/350; 536/23.1; 536/23.5

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	DURET et al. New insulin-like proteins with atypical disulfide bond pattern characterized in <i>Caenorhabditis elegans</i> by comparative sequence analysis and homology modeling. Genome Research. April 1998, Vol. 8, No. 4, pages 348-353, entire document.	1, 2, and 4-8
A	KONDO et al. Multiple gene copies for Bombyxin, an insulin-related peptide of the silkworm <i>Bombyx mori</i> : structural signs for gene rearrangement and duplication responsible for generation of multiple molecular forms of Bombyxin. J. Mol. Biol. 1996, Vol. 259, pages 926-937, entire document.	1, 2, and 4-8

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*G* document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

31 JANUARY 2000

Date of mailing of the international search report

22 FEB 2000

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
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Authorized officer

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Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/28315

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	LAGUEUX et al. cDNAs from neurosecretory cells of brains of <i>Locusta migratoria</i> (Insecta, Orthoptera) encoding a novel member of the superfamily of insulins. Eur. J. Biochem. 1990, Vol. 187, pages 249-254, entire document.	1, 2, and 4-8
A	SMIT et al. Growth-controlling molluscan neurons produce the precursor of an insulin-related peptide. Nature. 11 February 1988, Vol. 331, pages 535-538, entire document.	1, 2, and 4-8

Form PCT/ISA/210 (continuation of second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US99/28315

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 1
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

Claim 1 was not searched on the basis of sequence because SEQ ID NOs were not provided for the sequences of Figure 8. Claim 1 was searched to the extent possible using keyword searching.

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
1, 2 and 4-8

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet(1))(July 1992)*

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

WEST

Dialog (file: medicine)

search terms: insulin-like, insulin-related, protein, family, Drosophila, C. elegans, gene, mutate, mutation, mutant.

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claim(s) 1 and 2, drawn to a purified protein comprising an amino acid sequence of an A peptide domain and B peptide domain of a Drosophila insulin-like protein.

Group II, claim(s) 3, drawn to an antibody specific for a Drosophila insulin-like protein and not an insulin-like protein of another species.

Group III, claim(s) 4-8, drawn to an isolated nucleic acid encoding a Drosophila insulin-like protein, a host cell containing a vector encoding a Drosophila insulin-like protein, and a method of studying mutations in a Drosophila insulin-like protein gene.

Group IV, claim(s) 9, drawn to a knockout Drosophila melanogaster having a deleted D. melanogaster insulin-like gene.

Group V, claim(s) 10, drawn to transgenic animal containing a D. melanogaster insulin-like transgene.

Group VI, claim(s) 11, drawn to a compound screening assay for identifying a molecule that alters the expression level of a D. melanogaster insulin-like gene.

Group VII, claim(s) 12, drawn to a cell culture medium comprising a protein comprising at least 10 contiguous amino acids from a Drosophila insulin-like gene.

The inventions listed as Groups I-VII do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

The invention of Group I is distinct from the inventions of Groups II-VII because the inventions are drawn to materially different compositions and distinct methods. The protein of the invention of Group I is chemically, biologically, and functionally distinct from the antibody of the invention of Group II, the DNA and host cell of the invention of Group III, the knockout fly of the invention of Group IV, the transgenic animal of the invention of Group V, and the cell culture medium of the invention of Group VII. The invention of Group I is distinct from the invention of Group VI because the protein of the invention of Group I is not required to practice the method of the invention of Group VI, a compound screening assay that uses a transgenic fly cell.

The invention of Group II is distinct from the inventions of Groups III-VII because the inventions are drawn to materially different compositions and distinct methods. The antibody of the invention of Group II is chemically, biologically, and functionally distinct from the DNA and host cell of the invention of Group III, the knockout fly of the invention of Group IV, the insulin-like protein transgenic animal of the invention of Group V, and the cell culture medium of the invention of Group VII. The invention of Group II is distinct from the invention of Group VI because the antibody of the invention of Group II is not required to practice the method of the invention of Group VI, a compound screening assay that uses a transgenic fly cell.

The invention of Group III is distinct from the inventions of Groups IV-VII because the inventions are drawn to materially different compositions and distinct methods. The nucleic acid and host cell of the invention of Group III is chemically, biologically, and functionally distinct from the knockout fly of the invention of Group IV, the transgenic animal of the invention of Group V, and the cell culture medium of the invention of Group VII. The invention of Group III is distinct from the invention of Group VI because the nucleic acid and host cell of the invention of Group III is not required to practice the method of the invention of Group VI, a compound screening assay that uses a transgenic fly cell having a defined DNA construct encoding a reporter, not an insulin-like protein. The host cell of the invention of Group III contains a vector encoding an insulin-like protein, not a reporter molecule.

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The invention of Group IV is distinct from the inventions of Groups V-VII because the inventions are drawn to materially different compositions and distinct methods. The knockout fly of the invention of Group IV is chemically, biologically, and functionally distinct from the transgenic animals of the invention of Group V and the cell culture medium of the invention of Group VII. The invention of Group IV is distinct from the invention of Group VI because the knockout fly of the invention of Group IV is not required to practice the invention of Group VI, a compound screening assay that uses a transgenic fly cell.

The invention of Group V is distinct from the invention of Group VI because the transgenic animal of the invention of Group V is not required to practice the method of the invention of Group VI, a compound screening assay that uses a transgenic fly cell. The invention of Group V is distinct from the invention of Group VII because the insulin-like protein transgenic animal of the invention of Group V is chemically, biologically, and functionally distinct from the cell culture medium of the invention of Group VII.

The invention of Group VI is distinct from the invention of Group VII because the cell culture medium of the invention of VII is not required to practice the method of the invention of Group VI, a compound screening assay that uses a transgenic fly cell.

Accordingly, Groups I-VII are not so linked by the same or a corresponding special technical feature as to form a single general inventive concept.